BOOK OF ABSTRACTS

Island BIOLOGY

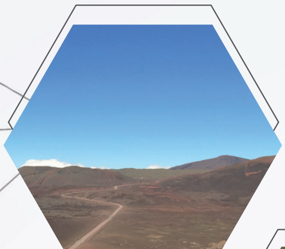
2019

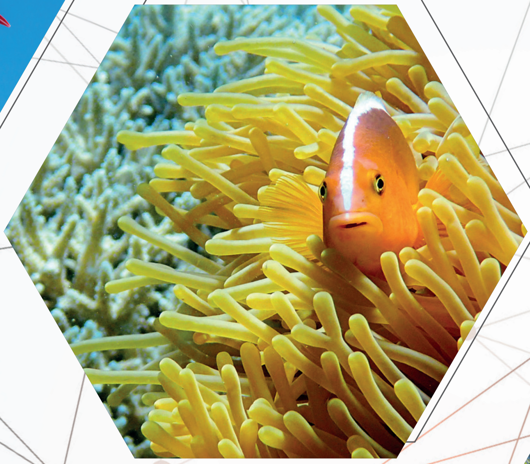
La Réunion

8-13 JULY

Université de la Réunion

Campus du Moufia





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Island Biology

Third International Conference on Island Ecology, Evolution and Conservation

8-13 July 2019

University of La Réunion
Saint Denis, France

BOOK OF ABSTRACTS

Editors:

Olivier Flores
Claudine Ah-Peng
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Description of contents

This document contains the collection of abstracts describing the research works presented at the third international conference on island ecology, evolution and conservation, Island Biology 2019, held in Saint Denis (La Réunion, 8-13 July 2019).

In the following order, the different parts of this document concern *Plenary sessions*, *Symposia*, *Regular sessions*, and *Poster presentations* organized in thematic sections. The last part of the document consists of an author index with the names of all authors and links to the corresponding abstracts. Each abstract is referenced by a unique number 6-digits number indicated at the bottom of each page on the right. This reference number points to the online version of the abstract on the conference website using URL `https://sciencesconf.org:ib2019/xxxxxx`, where `xxxxxx` is the reference of the abstract.

Table of contents

Marine Ecology 233

Marine Ecology 395

Palaeo-Biology / Palaeo-environments 407

Restoration Ecology / Ecological Restoration 412

Plenary Sessions

Introduction to natural history of the Mascarene islands

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Situated in the South West Indian Ocean, Mauritius, Rodrigues and Reunion are the main islands of the Mascarene archipelago. The Mascarene islands are often cited in textbooks as the home of the Dodo and as a place where human activities have resulted in mass extinctions and ecological disasters. Nevertheless, the archipelago still retains twenty-percent of its original habitats. The Mascarene biota is extremely diverse and most taxa have a high degree of endemism. Recent research studies in the Mascarenes allow a better understanding of the processes underlying evolutionary history and ecological patterns. Physical settings and biogeographical features make the archipelago similar to the Hawaiian Islands. A comparative analysis of the Mascarene biota with their analog on "Darwinian" islands is a promising avenue for detecting general rules and patterns and for exploring new and emergent questions in island biology.

Keywords: biodiversity, endemicity, hotspot, natural laboratory, remote archipelago

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The history, current status, and future of the protected areas of Madagascar

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The island of Madagascar is infamous for its exceptional biota with high levels of endemism at different taxonomic levels. Based on its separation from other landmasses in deep geological time, associated vicariance, and a nearly continuous history of subsequent colonization events, the fauna and flora of the island has few parallels in the world. Madagascar has a remarkable diversity of unique organisms, many micro-endemics, and a complexity of adaptive radiations. These aspects have been the themes of research for several decades and the importance of these biological splendors continue to be documented with continuous new discoveries, as well as this information being incorporated into on-going conservation programs. One of the critical aspects is that the vast majority of the terrestrial biota is forest dwelling. On the basis of a shifting sequence of factors ranging from traditional practices associated with slash-and-burn agriculture and creation and maintenance of cattle pasture, and the recent increase in commercial logging, the natural vegetation of the island has been greatly reduced. Further, different aspects of commercial exploitation of the country's mineral wealth are on the increase. Estimates indicate that less than 8-9% of the original forest cover remains and, most critically, the current terrestrial protected area system contains a large percentage of the enduring native forests. In 1989, Martin Nicoll and Olivier Langrand published a review of Madagascar's protected areas, and from a local or international perspective, this was a monumental advancement. Subsequently, several important aspects have changed for the positive, including a dramatic increase in the number of conservation sites, numerous conservation organizations working together to protect the remaining natural areas, enormous efforts to study and document the biota of the island, generations of national field biologists emerging, new perspectives on the evolutionary history, systematics, and ecology of a multitude of organisms, and something approaching an exponential growth in available information. On the negative side, particularly overlaid on population growth and economic problems, rates of deforestation have not notably decreased, fire remains an important problem, and different forms of natural resource exploitation are on the increase. In any case, all of these aspects provide the need to revisit the synthesis of Nicoll and Langrand. In this presentation, which is based on a recent large-scale review of 98 terrestrial protected areas of Madagascar, different historical aspects associated with the advancement of conservation on the island, and the status of the protected area system are given. The results of recent analyses within these protected areas associated with forest loss, problems with fire, and different forms of exploitation (removal of hardwoods, bush meat, etc.) are discussed. Contrasts are made between the pressures on different forest types and local cultural traditions. The final portion of the lecture addresses measurable advances in the protected area system, what we now know about the diversity of the islands vertebrates, and coherent plans for prioritization of continued biological exploration of the island.

Keywords: biodiversity hotspot, conservation, exploration, natural protected areas, resources

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The Island Biogeography of Alien Species

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Biological invasions by alien species – those transported by human actions to areas in which they do not naturally occur – represent one of the primary ways in which people are changing global biodiversity. Islands appear to be particular hotpots of alien species richness. This has been argued to reflect the greater invasibility of these locations, as a result of differences in how ecological processes such as interspecific interactions, underlying productivity or degree of disturbance act on islands versus continental mainlands. Variation in alien species richness has also been argued to provide insights into the patterns and processes structuring natural assemblages, because alien species are likely to follow some of the same laws as native species but break others. However, biological invasions are a consequence of a combination of factors - human actions, species characteristics, and environmental conditions - and so their study weaves together elements of history, biology, and geography. In this talk, I show why we would expect human actions to be the most important drivers of alien island biogeography, and why a failure to account for these is likely to lead to misleading conclusions about the causes of variation in the distribution and richness of alien species – even the question of whether islands are indeed more invasible than mainlands.

Keywords: Biological invasions, colonisation pressure, isolation, propagule pressure, species area relationship, species richness

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*Speaker

What can we learn about invasion ecology from ant invasions of islands ?

Lori Lach *† 1

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Nowhere are ecological communities more transformed by invasive species than on islands. The words 'islands' and 'invasive species' may evoke images of rats, cats, and goats preying on defenseless birds and mammals and devouring and trampling native plants. However, invasive ants have earned their place on the list of some of the world's most invasive species, and few, if any, inhabited tropical islands would have escaped invasion by one or more non-native ants or possibly even invasive ants. My talk will draw on results of multiple experiments investigating ant interactions with resident flora and fauna in insular and continental habitats and experience incorporating ant ecology into management actions and policy. From these experiences, I draw five broad lessons about ant invasions. 1) Context matters in determining the direction and magnitude of impacts. Ant populations will be dependent on access to resources, often plant-derived, and outcomes of their interactions will depend on which interactors are present and their role in the ecosystem. 2) Although context matters, knowledge of adverse experiences elsewhere is still a powerful motivating tool for management action, as it should be. Many of our best examples come from ant invasions of islands. Undoubtedly, this is partly because of 3) the 'simpler' floral and faunal compositions characteristic of islands. The lower species richness of islands means that they lack some of the functional redundancy that is characteristic of more speciose ecosystems. However, their relative simplicity also more readily enables characterization of the context of interactions and their impacts. Relatively depauperate biota have a modest capacity to buffer change, and therefore 4) island ecosystems are more dynamic than continental ecosystems. Changing conditions may eliminate or decrease the importance of some interactions but introduce or increase the importance of others. Some invasive ants weather these changes better than others. Therefore, islands may be the best place to investigate 'boom and bust' cycles. However, 5) though natural population declines of invaders are gaining attention, we cannot predict them, nor are they fast or certain enough to warrant complacency where invasive ants pose a threat to biodiversity. Looking to the future, islands can be important settings for trialing new techniques and novel methods for addressing problems posed by invasive ant species. Many of the lessons learned from ant invasions can be extended to other invasive biota.

Keywords: biological invasions, dysharmony, impacts, model taxa, taxon cycle

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Orchids, moths, and birds on Madagascar, Mauritius, and Reunion: island systems with well-constrained timeframes for species interactions and trait change

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The geologically young islands Mauritius (7–10 My) and Réunion (2 My), and the ancient continental island Madagascar, each harbor hundreds of species of orchids. Because orchid flowers have long fascinated biologists, their pollination has received more attention than that of other similarly species-rich tropical groups. An example is Darwin's famous prediction of a long-tongued moth pollinator for the long-spurred Madagascan orchid *Angraecum sesquipedale*. Over the past 10 years, field studies by ecologists from the Université de La Réunion and clock-dated molecular phylogenies for clades of orchids, passerine birds, and moths occurring on these islands, have provided time frames for changing pollinator / orchid interactions. In my talk, I will present data on both younger-than-expected and older-than-expected orchid pollinators (such as the moth species in Darwin's predicted *Angraecum / Xanthopan* trait-matching-system), and I will review what we now know about of the speed of change in plant / pollinator interactions on tropical islands compared to 20 years ago.

Keywords: evolution, interactions, molecular phylogenies, pollination, Tropics

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Ecology of rain forests on a large tropical island: lessons from New Guinea

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How tropical rainforests maintain their high biological diversity and how they regenerate after disturbance are two key, and related, questions of tropical ecology. I will explore these questions in the ecosystems of New Guinea, looking at the balance of bottom-up and top-down effects on biodiversity in rainforest food webs, and the dynamics of these effects along succession and elevation ecological gradients.

Keywords: biodiversity, food web, New Guinea, rainforest

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*Speaker

Symposia

A tale of two islands: Reunion and Kauai, similar conservation challenges and solutions (Symp.)

Contents

Integrating predator control efforts to achieve landscape level protections for native birds & their habitats on Kauai Island

Sheri Mann *† [1,2]

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Non-native predator introductions to island ecosystems have happened around the world throughout history and there are many examples of the devastation that introduced predators can cause if left unchecked. There are also many examples of successful eradications and/or significant suppression of introduced predators. In almost all cases, it takes a tremendous amount of effort, money, coordination, persistence and partnerships to achieve eradication and significant suppression. All too often, however, efforts are disjointed and rarely is data/results from multiple efforts shared or used to teach us what we need to know in order to understand predator behaviour, so we can maximize efforts and efficiencies. Non-native predators are a constant threat to Kauai's forest, sea, water, shore and wading bird populations. Feral cats, Black rats, Polynesian rats, Norwegian rats, Cattle Egrets, Barn owls, feral pigs, mosquitos and more predate and/or harm native birds, which reduces their survival and reproduction potential. Some feral cats also carry Toxoplasmosis, which has been found in dead marine animals near Kauai including Monk seals, dolphins and whales, and in one human baby. Rats, pigs, goats and deer also contribute to habitat destruction through seed predation, plant destruction, non-native seed distribution and creating habitat for invasive mosquitos. This presentation will describe a new approach that more closely brings resources and partnerships together to control non-native predators across Kauai's landscapes. This will be accomplished by simplifying onerous procedures often associated with multiple funding sources and reporting, as well as capitalizing on shared goals and resources through more collaborative approaches that bolster research, technology development, access agreements, shared funding and educational outreach.

Keywords: landscape level restoration, predator control

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Improving effectiveness of alien plant clearing on Reunion Island through partnership

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Biological invasions threaten biodiversity worldwide, especially on tropical islands such as Reunion Island. Here we present the results of a collaborative effort to map biodiversity priorities and to prioritise alien plant clearing. We first combined all existing data on habitats, threatened and endemic species and the distribution of alien plant species. Using expert-knowledge where necessary, we provide the first map of invasion level for the whole island. We developed a decision-making process using Zonation, a conservation-planning tool, to identify biodiversity conservation priorities. Conservation priority areas were selected to maximise biodiversity levels in areas lightly invaded. We then included criteria to identify priority areas for alien plant clearing based on clearing costs, accessibility and history of previous clearing programmes. Almost 40% of the remaining natural habitats on Reunion Island are moderately to heavily invaded. We identify 58,500 ha as conservation priority areas of which 30% are considered to be not invaded at all. We discuss how this will impact future alien plant clearing programmes and propose the basis for an integrated clearing and restoration plan for Reunion Island.

Keywords: Alien species, conservation, planning tool, partnership

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Race against time: research and conservation efforts to save Kauai's endangered song birds

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The Hawaiian Islands are facing an extinction crisis. On Kauai Island, five songbird species disappeared in the last 50 years. Three critically endangered species number Culex mosquitoes, an important disease vector. Thus, we used LiDAR (Light Detection And Ranging) imagery and automated recording devices (ARD) to produce habitat suitability maps to spatially target conservation actions on a landscape scale on Kauai. Using detections and nest locations of endangered Akikiki and Akekee from 2012-2017, we identified LiDAR-derived attributes associated with presence and nest sites. Both species nested in areas where mean canopy height was ≈10 m. Presence was most strongly associated with canopy height, elevation, and slope. To groundtruth habitat maps, in 2017-8, we deployed ARDs on 12 transects for 2-4 week periods and conducted Variable Circular Point Counts and area surveys to determine distribution and densities of forest birds and find nests. Using these approaches, we located unknown concentrations of all three endangered forest bird species of Kauai that we can target for protection. Simultaneously, we founded conservation breeding populations of Akikiki and Akekee by collecting eggs and transferring them to breeding facilities. Akikiki currently number 46 individuals in captivity and have started breeding; Akekee number 10 birds. We have deployed 425 self-resetting rat traps at two sites to protect crucial nesting habitat from predation, resulting in a 4-fold decrease in rat abundance. Partner agencies have fenced hundreds of hectares of habitat to avert ungulate damage. Furthermore, we are investigating *Culex* distribution and demography at two sites. As we find *Culex* larvae, we control them locally with Bti; more importantly, distributional and demographic data will inform landscape control using sterile *Culex* in the near future. Collectively these actions hold the promise of saving Kauai's birds from extinction. We discuss lessons learned that may be valuable to those faced with similar situations.

Keywords: endangered, habitat suitability modeling, Hawaii, honeycreeper, predator control

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*Speaker

LIFE BIODIV'OM – An ambitious program (2018 – 2023) for the conservation of a critically endangered forest bird , the Reunion Cuckooshrike

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The Reunion Cuckooshrike or Tuit-tuit (Lalage newtoni) is an endangered species whose global population is estimated at only 40 breeding pairs (SEOR, 2017). Between 1974 and 2005, monitoring of their numbers showed a drop of almost 25% in the number of singing males on the Roche Écrite massif. In 2006, bird counts carried out by the Réunion Society for Ornithological Studies (SEOR) revealed that the species was on the brink of extinction, with only 11 pairs dispatched in an area of less than 10 km^2. In 2004, following several predation tests, the Réunion Society for Ornithological Studies (SEOR) identified the rat (*Rattus rattus*) as being the predator with the highest impact on this species. Since then, rat control compaigns have been implemented to limit the impact of the predator during the breeding season. Since 2004, SEOR, Réunion National Park, and the French National Forestry Agency (ONF) have been testing a streamlined method using "Mini Philproof" rat bait stations and rat bait scattered on both sides of the transects using slingshots. Every year, the population and reproductive success of this species are monitored throughout its distribution range, which allows us to check the efficiency of the different rat control methods used over the past 15 years. Rat control remains the key action to guarantee the future of this species and the new challenge is to continue this operation during the next decade. In 2018, an ambitious and multi-faceted program, called LIFE BIODIV'OM, was initiated to engage massive conservation actions with a translocation project on this critically endangered species and a large program of rat/cat/Red-Whiskered bulbul control with local volunteer mobilization over 10 years time and covering 1500 ha.

Keywords: Conservation, Reunion Cuckooshrike, predators control

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*Speaker

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Human caused mortality crisis for the endangered seabirds of Kaua'i: quantifying the impact of power line collisions and light attraction

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On Kaua'i, both the Newell's Shearwater and Hawaiian Petrel are vulnerable to power line collisions, because they make frequent nocturnal flights crossing power lines, and light attraction which grounds fledglings during their first flight to sea. To determine the impact of power line collisions, we have conducted 6,091 hours of observations from 2012-2018 quantifying seabird power line collisions, flight height, and behavior at power lines. We also developed a novel monitoring tool - automated acoustic surveys of avian power line collisions - which has dramatically increased the temporal and spatial scale of monitoring (276,879.5 total hours), overcoming many of the biases inherent in traditional bird carcass counts. Based on our observations, we report that 9.3-15.3% of seabird power line collisions result in an immediately grounded bird and use this as a proxy for minimum mortality. Automated acoustic surveys at a sample of sites along the entire power line grid detected a total of 8,715 collisions over six years. We developed a statistical model to predict collision risks across the island-wide transmission wire grid and estimated a total of 10,552 collisions per year, with a minimum mortality of between 981-1,614 endangered seabirds annually. We validated our model estimates both statistically and with orthogonal data sets. The acoustic results are fully supported by both downed bird results and a separate mechanistic model utilizing observations of seabird collisions and passage rates at power lines. The observer model fit seabird collisions to observational data, incorporating powerline characteristics as well as spatial, temporal, and environmental covariates to asses risk. These results show that power lines collisions are the largest documented source of mortality for two endangered species shown to have undergone a large-scale population declines on Kaua'i. To determine the impact of light attraction, we conducted 7,500 km of surveys looking for grounded juvenile birds. We found a mortality rate of 35-43% for grounded birds, and discovered that dead birds were rarely reported by the public. Given that Kauai residents have found $>$ 30,000 live birds since 1979, we estimate that unreported mortality was between 16,100-22,600 seabirds over the same time period.

Keywords: light attraction, power line collisions, seabird mortality

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Unexpected advances for endangered endemic petrels conservation on Reunion Island

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Reunion Island (western Indian Ocean) is one of the islands in the world holding two endemic species of petrels, the Barau's Petrel (*Pterodroma baraui*), and the Mascarene Petrel (*Pseudobulweria aterrima*), both of which are poorly known and endangered. The principal threats to both species are introduced mammalian predators (rats and feral cats) and impacts of light pollution. The Mascarene Petrel has a very restricted population (between 45 and 400 pairs, with an average estimate of 250 pairs). This species is the most endangered endemic seabird of Reunion Island, and one of the rarest seabirds in the world. Remarkably, the breeding colonies for this critically endangered species remained unknown until late 2016, just over two years ago. How could breeding colonies of a species of global conservation concern be unknown for so long? It is due to a combination of factors, including a very small population size, the fact that Mascarene Petrels nest in underground burrows and only visit their colonies at night, and the incredibly rugged, steep, mountainous and heavily vegetated interior of the island where the petrels nest. Since 2015, an ambitious and multi-faceted program, called LIFE+ PETRELS, was initiated to engage massive research and conservation actions. Indeed, in less than 3 years, 2 breeding colonies of Mascarene Petrels were discovered, and more than 45 nests were monitored with 70 individuals, allowing the team to study biology and ecology of this elusive species. In this talk, we propose an overview of all the incredible results obtained within the LIFE+ PETRELS project and share innovative strategies and creative techniques, both on the breeding colonies and with local human communities on Reunion, to address a multitude of threats to the long-term conservation of these two single-island endemic species.

Keywords: Mascarene Petrel, conservation, LIFE+, Réunion Island

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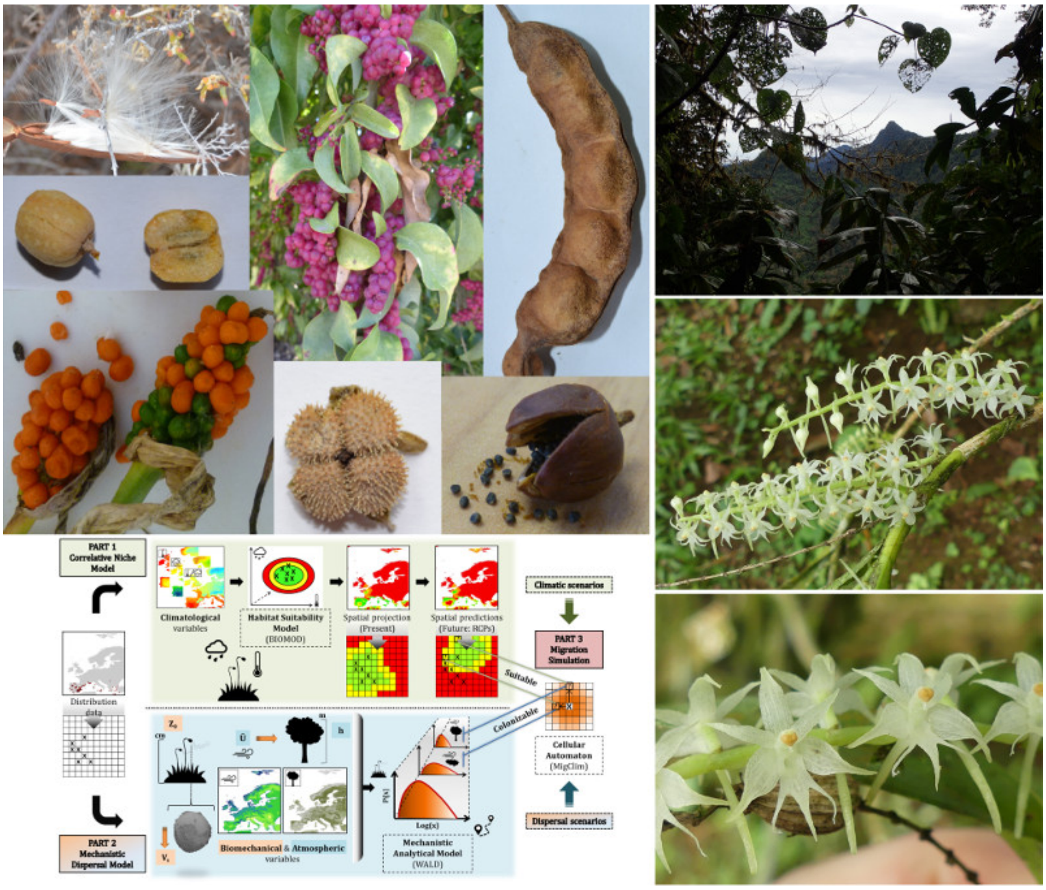
*Speaker

Dispersal ecology meets island evolution (Symp.)

Contents



You move, I change: model-based approaches reveal striking differences between the evolution of plants and animals in the Canary Islands

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We assembled published molecular and phylogenetic data for a wide range of terrestrial animal and plant groups occurring in the Canaries to study similarities and differences in how their diversity on the islands originated. In total, we analysed 20 animal clades (383 taxa, 659 sequences) and 16 plant clades (449 taxa, 659 sequences). For each clade, we partitioned the molecular dataset by type of marker and applied different molecular rates. Clock and dispersal rates were also allowed to differ among clades. We used discrete-state continuous-time Markov chains to model how different lineages colonized the islands and subsequently moved between islands and habitats as they diversified. We used the phylogenetic graphical model framework introduced in RevBayes to modify the structure of the biogeographic rate matrix, such that we could tease apart different factors (area, geographic distance, age) influencing the relative carrying capacities and exchangeability rates. Inference was based on Bayesian Markov chain Monte Carlo analyses that integrated out uncertainty concerning phylogenetic relationships and all molecular and biogeographic model parameters. Our results show that inter-island dispersal rates and island carrying capacities (equilibrium number of lineages) do not correlate with geographic distance or island size. Carrying capacities in plants are lower for all islands but higher for the mainland compared to animals. Plant lineages move between islands faster than animal lineages, though inter-island dispersal patterns are similar. Plants shift between islands more readily than they shift between habitats, whereas the reverse is true for animals; when animals move between islands, they often shift to a new habitat. The proportion of the island's carrying capacity that is not dependent on island area is larger in animals than in plants, suggesting a larger role for environmental heterogeneity. Conversely, dispersal rates, after partitioning out geographic distance, are higher in plants than in animals. We conclude that in the Canary Islands, animals have a tendency to diversify locally into different ecological habitats, but rarely colonize new islands. In contrast, plants move readily between islands but rarely shift habitat. This agrees with observed patterns at continental scale and points to interesting conclusions about community assembly on islands.

Keywords: Animals, Bayesian inference, Canary Islands, carrying capacities, dispersal rates, island biogeography, plants, phylogenetic graphical models, RevBayes

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[*] Speaker

Dispersal, niche and topoclimatic variation: speciation consequences for island invertebrates

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Understanding speciation as a process on islands, particularly speciation within individual islands, is key to explain the high levels of invertebratespeciation that characterise many oceanic islands and archipelagos. Radiations of invertebrategenera, whether presumed to be adaptive or non-adaptive, have been the subject of a rich history of molecular phylogenetic analysis, revealing both the geography and timing of speciation at the archipelago scale. However, there has been rather less focus on the process of speciation itself, particularly speciation within islands. A key focus of our research in recent years has been to investigate how spatial variation in climate within islands can catalyse speciation by disrupting gene flow. In this talk I will present results from two mutually informative studies led by our group. The first is a clade-level approach within a diversified weevil genus across the island of Gran Canaria. The second is a community-level approach at a much smaller spatial scale within the laurel forest of Tenerife. Results from both studies emphasise the interaction of topography and changes in climate throughout the Quaternary as a driver of speciation, mediated by species-specific dispersal and niche characteristics. By combining RAD-seq data with high resolution climate models, we show that when dispersal ability and ecological tolerances are restricted, microclimatic variation over distances of only a few kilometres can maintain strong geographic isolation and drive speciation.

Keywords: Quaternary, diversification, insect, arthropod, RAD, seq, population genetics

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*Speaker

Defining geographical island isolation for terrestrial mammalian dispersal

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Geographical isolation is often invoked to facilitate biogeographic enquiry. General practice of elucidating isolation through *ad hoc* species richness metrics may not properly inform such concepts, though. Here we addressed this problem by defining geographical insular isolation for dispersing terrestrial mammals, using a multivariate characterisation of contemporary and conventional metrics explaining species richness. This study was conducted on the 890 offshore islands ($\geq$ 1 hectare) of the New Zealand archipelago (latitude: 34.1-47.3$\circ$S, longitude: 166.2-178.4$\circ$E). Principal components analysis (PCA) was used to reduce dimensionality of the island dataset, thereby creating composite variables (principal components, PCs) characterising the primary drivers of insular isolation. An amalgamation of 16 variables were considered, including: Euclidean-based distance measurements, stepping-stone sequences, landscape measures of isolation, graph-theoretic metrics, and island area. For each island, relevant variables were quantified in a context-specific manner matching the life-history of specific dispersing species. Distance from the mainland (PC1 Distance) and the number of stepping stones utilised *en route* (PC2 Stepping Stones) comprised 72.2% dataset variance. PC1 Distance explained over half of New Zealand's isolation alone, and multiple variables had high factor loading scores. Focal island area (PC3 Area) was only marginally important, comprising 7.3% dataset variance. Based on dataset variance, PC1 Distance and PC2 Stepping Stones suitably characterised insular isolation for New Zealand, reaffirmed through parallel analysis and Kaiser's criterion. Moreover, a simple Euclidean distance measurement is likely sufficient when quantifying PC1 because it describes distance from the mainland equally well as other methods, including graph-theoretic least-cost and circuit theory methods, in a much simpler manner. This depiction can be used to facilitate subsequent biogeographic enquiries characterising isolation because the demonstrated metrics were substantiated.

Keywords: geographical isolation, offshore islands, principal components analysis, mammal dispersal, New Zealand

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Tridactyle (Orchidaceae): a story of speciation and colonisation in São Tomé and Príncipe.

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Despite many zoological biogeographic studies on the islands of the Gulf of Guinea, the mechanisms of diversification are still poorly understood, and almost no studies have been conducted on the origin of the flora. Here, we used the genus *Tridactyle* (Orchidaceae) (50 spp.) as a model to understand the story of colonization of epiphytic orchids. This genus is only found in continental Africa and São Tomé and Príncipe, and has a very high rate of endemicity on these islands. Resolving phylogenetic relationships allowed to investigate how species diversity has evolved on this archipelago, and more precisely, we tested three main colonisation scenarios that could explain the diversity of *Tridactyle*: i) a scenario of colonisation without speciation, ii) adaptative radiation and iii) a simultaneous colonisation by taxonomically and/or ecologically linked organisms. In this study, we used one nuclear maker *PhyC* (c. 900 pb), the sequencing of plastome (pDNA: c. 160,000 bp), ribosomal DNA (rDNA: c. 5900 bp), and habitat characteristics for each species (41 species), which provided: (i) a phylogenetic relationships tree between species and estimated the divergence period between the main lineages, and (ii) reconstructed ancestral states regarding biome preferences. Preliminary results suggested than the adaptative radiation was the most probable scenario, with one species, *Tridactyle tridactylites,* colonizing both islands and differentiated with elevation and habitats.

Keywords: São Tomé and Príncipe, Gulf of Guinea, Tridactyle, Orchidaceae, radiation, ecological differentiation.

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*Speaker

Evolutionary trends in island plants: is everything lost on islands? (Symp.)

Contents

The loss of size diversity in island plants

Kevin Burns *† [1]

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Animals that evolve on isolated islands break all the rules. Speedy, nervous, little birds repeatedly become plump, tame and flightless. This symposium asks whether plants evolve similar patterns in dispersal ability, size and defence on islands. It also asks whether they display additional evolutionary trends on islands, including differences in gender and floral biology. In the first part of my presentation, I outline the types of repeated patterns in evolution we might expect to observe in island plants, many of which will be considered in detail by the symposium speakers. Next, I test for the loss of size diversity in island plants using a dataset from islands in the Southwest Pacific. I specifically test for evidence of the 'island rule' in leaf area, plant stature and seed size. Results showed that taller plants with bigger leaves repeatedly evolved to become smaller on islands, while shorter plants with smaller leaves evolved to become larger. Therefore, leaf area and plant stature obeyed the 'island rule' and exhibit a loss of size diversity. On the other hand, seeds regularly increased in size on islands, regardless of their size on the mainland, providing a striking example of convergent evolution. By establishing what is currently known about repeated patterns in the evolution of island plants, including the loss of size diversity, this symposium provides a first step towards understanding repeated patterns in the evolution of island plants.

Keywords: evolution, island syndrome, leaves, plant, seeds, stature

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Loss of defenses on island plants: from theory to evidence

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Many types of herbivores are rare or absent on islands. It has therefore been hypothesized that insular plants are more poorly defended than their mainland counterparts. However, this hypothesis has been questioned by recent work reporting no evidence of such trends or even increased chemical defense in island systems. In this talk we: (i) synthesize potential sources of inconsistency in the study of insularity effects on plant-herbivore interactions; and (ii) outline experimental approaches that may help us to address major limitations in island-mainland comparisons of plant defense. To this end, we emphasize the cornerstone idea that plant defense is a complex trait stemming from different types of phenotypic responses, including those developed after herbivore damage (i.e. induced defenses) or those mediated by indirect associations with third trophic levels (i.e. indirect defenses). We also highlight the role of abiotic (e.g. climatic) factors, which has been largely neglected in studies of insular plant defense despite marked differences in habitat conditions between source (continental) and island regions. Finally, we identify the lack of a comprehensive spatio-temporal framework as a fundamental drawback for data interpretation in island evolutionary studies on plant defensive traits. In summary, island-mainland systems provide a unique experimental setting for evolutionary studies on plant defense, but our analyses and conclusions may benefit from considering key ecological and phylogeographical factors related to plant-herbivore interactions.

Keywords: chemical responses, island vs. mainland comparisons, island syndrome, phylogeography, plant defence, plant–animal interactions

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*Speaker

Are genetic diversity patterns cogent with a generalized loss of dispersal in island plants? Insights from Macaronesia

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Classical island biodiversity theory predicts that insular populations generally have limited stocks of genetic diversity. However, notable exceptions to this hypothesis started to appear since the seminal applications of molecular techniques to the investigation of island endemics, and have experienced an upward surge in recent times due to both the thorough consideration of diversification processes in widespread insular lineages, and the inception of new generation genetic analysis techniques. At odds with the classical tenets of island biogeographical theory, abundant evidence based on consistent populational and genetic sampling in multi-island oceanic archipelagoes is revealing complex diversification landscapes where plant endemics often display great genetic diversity levels, directly related to the maintenance of high dispersability capabilities. In tight connection, phylogeographical analyses are also describing very dynamic scenarios of frequent inter- and intra-island colonization, and complex patterns of hybridization that underlie the origins of some conspicuous island radiations, and often reveal the existence of (i) ongoing speciation processes at local spatial scales (‘islands within islands’), and (ii) glaring incongruences with the currently accepted taxonomy. The talk will assess genetic data to showcase discrepancies between the classical island genetic diversity theory and the emerging picture, emphasizing the ensuing conservation implications. Our main focus will be the Canarian archipelago, where the sharply different ontogenetic stages of the different islands, their climatic stability during Quaternary glacial cycles, and their great closeness to the mainland have likely promoted a much higher incidence of processes that conflict with some important tenets of the island syndrome.

Keywords: genetic diversity, Canary Islands, widespread lineages, NGS, island syndrome

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Loss of pollination syndromes after island colonization

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In his renowned book "On the origin of species", Charles Darwin predicted the fantastic co-evolution of the plant-pollinator relationship that would have taken place between Angraecoides orchids and a giant hawkmoth (sphingid) on Madagascar. Since then, the study of pollination biology has been a major theme in the Madagascan region. This is a hotspot of biodiversity composed by the main island of Madagascar and surrounding archipelagoes (Comoros, Seychelles and Mascarene). Biogeographic evidence suggests that most of the Mascarene island colonists have a Madagascan origin, which imposes a 800 km sea barrier to dispersal. Such a filter is reflected by the underrepresentation of animal elements when compared to the source area, with insect pollinators being no exception. One of the main objectives of our research over the last 10 years has been to answer the following question: how did the angrecoids-sphingid relationships evolve after colonization of the Mascarene archipelagoes? The main conclusion is that a great variability has been generated during the evolution of this syndrome under island isolation. In some cases, the pollination system is maintained, but in other cases it is lost in favor of selfing, finality pollinator shift occurs in lineage and gave raise to new pollinator syndromes.

Keywords: Mascarene evolution, orchids, pollination, sphingid

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*Speaker

What do wind-dispersed species tell us about loss of dispersal potential on islands?

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Recent island colonists are expected to represent the fraction of the mainland source population with greater dispersal ability. After colonization, the loss of dispersal on islands hypothesis (LDIH) predicts that island populations will experience a rapid reduction in dispersal ability due to negative selective pressures imposed by loss of propagules at sea. Several classic and contemporary works have supported these predictions, with study cases focusing mainly on plants and flightless animals with restricted endemic island or island-like distributions. Less effort, however, has been made to address these predictions using island endemic lineages that have successfully colonized multiple islands. Within these lineages, anemochory provides a prime study system because it allows for testing of the evolution of dispersability from a mechanistic point of view, e.g. based on morphological features of fruits and seeds. Additionally, providing a spatio-temporal framework may prove useful for testing how island population age relates to evolutionary trends in dispersal-related traits. Thus, combining phenotypic plant traits and phylogeographic analyses, I will present several studies that have failed to find evidence of dispersability loss in different island lineages. I will discuss how these results could be potentially attributed to factors such as habitat availability, colonization age or selection for seed size increase on islands. Additionally, I will show examples where dispersal traits are poorly conserved phylogenetically, and that there is a need to test both phylogenetic signal and the level of niche conservatism to infer the evolution of dispersability. Altogether, these studies failed to support the central predictions of the LDIH, which calls for a redefinition of the factors driving the evolution of wind-dispersal traits on islands.

Keywords: plant evolution, dispersability, phenotypic plant traits, phylogeography, diaspores

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*Speaker

Functional island biogeography - concepts and prospects (Symp.)

Contents

Functional island biogeography: the next frontier in island biology

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Island biota exhibit a fascinating diversity of form and function, and the specular morphological and behavioral oddities of island species compared to mainland relatives have received considerable scientific interest. Interestingly, all influential theories in island biogeography including the Equilibrium Theory and the General Dynamic Model of Island Biogeography do not consider such differences in species traits but instead treat all species as functionally equivalent. Such an ecologically neutral perspective clearly represents an oversimplification of the nature of island biota and limits our ability to understand the complex interplay of processes underpinning the distribution and diversity of island species and to predict how island species are affected by global environmental change. The large body of literature that exists on traits associated with dispersal and colonization, island syndromes (e.g. derived island woodiness, disharmony) or convergent trait evolution on different islands, however, currently lacks a coherent framework. Here, we argue that islands are particularly suited for a trait-based approach to study how different dispersal and environmental filters shape species assemblages at different spatial scales and how functional diversity emerges over time. We propose functional island biogeography, as an emerging sub-discipline that studies the distribution and composition of traits and functional diversity of island organisms across different organizational levels, and argue that this approach has great potential to link currently disparate areas of island research at the interface of functional ecology, biogeography and evolutionary biology. Moreover, functional island biogeography might offer new insights into the consequences of species losses and introductions on the functioning or island ecosystems. Building on recent case studies, we show how functional island biogeography can take advantage of existing eco-informatics tools, databases, and standardized field sampling protocols and how this opens new avenues of research by integrating information about species distributions, abundances, and functional traits.

Keywords: island syndromes, functional diversity, functional island biogeography, traits

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*Speaker

A global review of insular woodiness and its potential functional significance

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The repeated evolution of woody growth form in herbaceous lineages on islands—insular woodiness—has long been recognized as an iconic island phenomenon. Several hypotheses exist on the drivers of the evolution and the adaptive value of derived woodiness on islands, including amongst others the release from climate seasonality and herbivore pressure. However, experimenting studies supporting these hypotheses are virtually absent and a synthetic global view on the biogeography and of correlates of derived insular woodiness is missing so far, mainly because there has been no global overview available on the identity and geographical distribution of derived woody species. Here we present a novel global derived woodiness database and combine it with the Global Inventory of Floras and Traits (GIFT), georeferenced species occurrences, and environmental data in a generalized linear modeling framework to identify global diversity patterns of derived insular woodiness and potential environmental correlates. Specifically, we test the fraction of derived woody species in the flora of oceanic islands globally and relate it to island characteristics including island age and isolation, climate, and herbivore presence. The results show a large difference in importance of derived woodiness across islands, supporting several archipelagos known for derived woodiness as diversity hotspots, especially Hawaii and the Canary Islands. Climate emerged as an important correlate of derived woody species diversity, across latitudes. However, the results suggest taxon-specific drivers among evolutionary lineages. In summary, we introduce a novel dataset on derived insular woody species and provide our first results on a global perspective on the biogeography and correlates of insular woodiness.

Keywords: insular woodiness, global biogeography, climate

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*Speaker

Drivers of woody alien invasions across spatial scales in the Hawaiian Islands

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Islands harbor a disproportionate amount of global plant diversity, emerging as a result of isolation and dynamic geophysical processes. However, isolation also facilitates alien invasions of islands, potentially changing community structure, displacing endemic species, and threatening the provisioning of vital ecosystem services. It is therefore critical to deepen current understanding of the factors that allow alien species to successfully establish in and dominate native forests on islands. Here we assess shifts in the relative importance of abiotic and biotic drivers, and their interactions, on the establishment and dominance of alien species across spatial scales in the Hawaiian archipelago. We used a database of more than 450 forest plots to examine patterns of woody plant invasions at local ($<$ 1 ha) and regional scales (10,000 ha). We calculated phylogenetic distinctiveness (PD) of woody alien species as the mean phylogenetic distance to the nearest native species. We also gathered wood density and seed mass data for alien species to explain variation in their establishment and dominance. At each spatial scale, we fit phylogenetic multilevel Bayesian models to examine variation in establishment and dominance of alien species as a function of biotic (e.g., PD, wood density, and seed mass) and abiotic factors (e.g., precipitation, potential evapotranspiration (PET), soil age, and the human influence index (HII)) and their interactions. At the regional scale, we found that the probability of establishment increased with PET and that phylogenetically unique alien species were more likely to establish in areas with young soils or low precipitation, while those with heavy seeds established well in areas with high precipitation. At the local scale, the establishment of alien species was positively associated with PET, soil age, and HII. However, alien species exhibited different rates of establishment along gradients in precipitation, PET, and soil age that were strongly modulated by species' phylogenetic uniqueness, wood density, and seed mass. Local dominance of alien species also was strongly context dependent; all biotic factors exhibited significant interactions with HII. Our results show that where woody alien species occur or where they are dominant is contingent upon the joint effects of abiotic and biotic filtering.

Keywords: biological invasions, spatial scales, forests, functional traits

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*Speaker

Predicting the functional trait composition of insular communities: an application to tropical reef fishes

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The Theory of Island Biogeography (TIB) predicts how area and isolation, through colonization and extinction dynamics, influence species richness equilibrium on insular habitats.However, the TIB remains silent about functional trait composition and provides no information on the scaling of functional diversity with area, an observation that is now documented in many systems. To fill this gap, we develop a probabilistic approach to predict the distribution of a trait as a function of habitat area and isolation, extending the TIB beyond the traditional species–area relationship. We then compare model predictions to the body-size distribution of piscivorous and herbivorous fishes found on tropical reefs using a database compiling the presence/absence of 991 reef-associated fishes in 134 locations worldwide. We find that small and isolated reefs have a higher proportion of large-sized species than large and connected reefs. We also find that knowledge of species body-size and trophic position improves the predictions of fish occupancy on tropical reefs, supporting both the allometric and trophic theory of island biogeography. The integration of functional ecology to island biogeography is broadly applicable to any functional trait and provides a general probabilistic approach to study the scaling of trait distribution with habitat area and isolation. This framework open new perspectives in the fields of macroecology, functional ecology and biodiversity management since it highlights the potential impact of habitat destruction and fragmentation on the functional reorganization of species assemblages.

Keywords: island biogeography, functional traits, tropical reefs, allometric theory

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[*] Speaker

Extinction-Driven Changes in Insular Frugivore Communities: Worldwide and in Mauritius

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Global change and human expansion have resulted in many species extinctions worldwide, but the geographic variation and determinants of extinction risk in particular guilds still remain little explored. Here, we quantified insular extinctions of frugivorous vertebrates (including birds, mammals and reptiles) across 74 tropical and subtropical oceanic islands within 20 archipelagos worldwide and investigated extinction in relation to island characteristics (island area, isolation, elevation and climate) and species' functional traits (body mass, diet and ability to fly). Out of the 74 islands, 33 islands (45%) have records of frugivore extinctions, with one third (mean: 34%, range: 2–100%) of the pre-extinction frugivore community being lost. Geographic areas with more than 50% loss of pre-extinction species richness include islands in the Pacific (within Hawaii, Cook Islands and Tonga Islands) and the Indian Ocean (Mascarenes, Seychelles). The proportion of species richness lost from original pre-extinction communities is highest on small and isolated islands, increases with island elevation, but is unrelated to temperature or precipitation. Large and flightless species had higher extinction probability than small or volant species. Across islands with extinction events, a pronounced downsizing of the frugivore community is observed, with a strong extinction-driven reduction of mean body mass (mean: 37%, range: –18–100%) and maximum body mass (mean: 51%, range: 0–100%). The results document a substantial trophic downgrading of frugivore communities on oceanic islands worldwide, with a non-random pattern in relation to geography, island characteristics and species' functional traits. This implies severe consequences for ecosystem processes that depend on mutualistic plant–animal interactions, including ecosystem dynamics that result from the dispersal of large-seeded plants by large-bodied frugivores. We suggest that targeted conservation and rewilding efforts on islands are needed to halt the defaunation of large and non-volant seed dispersers and to restore frugivore communities and key ecological interactions.

Keywords: Community, Extinction, Frugivores, Macroecology, Biogeography

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Future steps to fight against invasive species on islands (Symp.)

Contents

The new IUCN Guidelines for invasive species planning and management on islands

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Activities to avoid or mitigate negative impacts of invasive species are seen as high priority on islands. A new IUCN publication provides guidelines for such activities. It is available in three languages: English, French, and Spanish. The talk will focus on and provide examples for the aims of the guidelines which are designed to assist anyone planning and programming invasive species management on islands. These aims are, i.a., to provide a comprehensive framework for invasive species management on islands,address all problem areas and facilitate prioritisation,increase action and improve implementation,increase efficiency and cooperation and reduce duplication, guide the work of international and regional agencies incl. donors, guide the development of country and island programs, including National Invasive Species Strategies and Action Plans and individual agency plans, and guide strategic and local fundraising. The two sections of the guidelines will also be presented: a 'Checklist' section and a 'How to' section. The Checklist' section presents essential components of a comprehensive and effective invasive species management program, arranged in ten Thematic Areas, and grouped into three overall Themes (Foundations; Information and Prioritization; Management Action). All 10 Thematic Areas need to be considered when planning an invasive species programme for an island or islands. The 'How to' section, provides supplementary guidance on the planning and implementation process, mainly on how to engage, build momentum and support, make decisions, prioritise, and translate plans into action. The Guidelines may be used at a local, national or regional level. Best practice example for the utilization of the Guidelines are shown, because not every country or agency needs to do everything. The Guidelines facilitate prioritisation by country, territory, island or agency, and help to ensure that key aspects relevant to any given situation or programme are not forgotten. As objectives are not prioritised, each stakeholder can select those objectives that it considers important for its own programme. Based on a "user-focussed" presentation, the utilization of the Guidelines for the mitigation of negative impacts of invasive species on islands in-situ and ex-situ shall be encouraged.

Keywords: invasive alien species, management actions, ex situ / in situ conservation

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Island Biodiversity in the Anthropocene

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Biodiversity on oceanic islands is characterised by unique biogeographic, phylogenetic and functional characteristics. Islands hold a disproportionate amount of the world's biodiversity, and they have also experienced a disproportionate loss of it. Following human contact island biodiversity has sustained negative human impacts increasing in rate and magnitude as islands transitioned from primary, through secondary to tertiary economies. In contrast to continents, on islands habitat transformation and invasive species have historically been the major threats to biodiversity, and although these threats will continue in new forms, new impacts such as climate change are emerging. Islands thus are microcosms for the emerging biodiversity and socioecological landscapes of the Anthropocene. Islands will require novel strategies for their protection and restoration, including mainstreaming biodiversity in cultural and production landscapes and incorporating novel ecosystems, but they present great opportunities to do so.

Keywords: Anthropocene, biodiversity, nature conservation, novel ecosystem, invasive species, oceanic island

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*Speaker

Predicting and preventing the arrival of invasive non-native species on islands globally

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Biological invasions can threaten biodiversity and ecosystems, particularly through their interactions with other drivers of change. There are many examples of the adverse effects of invasive non-native species from islands which seem to be particularly vulnerable to the threat of biological invasions. It is widely recognised that preventing the most damaging invasive non-native species arriving within a new region is the most effective management strategy. However, predicting invasions is difficult. Horizon scanning, the systematic examination of future potential threats and opportunities, leading to prioritization of invasive non-native species threats, is seen as an essential component of invasive non-native species management. We developed an approach which coupled consensus methods (which have previously been used for collaboratively identifying priorities in other contexts) with rapid risk assessment. The process involved two distinct phases: 1. Preliminary consultation with experts within distinct groups (plants, invertebrates, vertebrates and marine species) to derive ranked lists of potential invasive non-native species. 2. Consensus-building across expert groups to compile and rank the entire list of potential invasive non-native species. Over the last year we have implemented this approach across the UK Overseas Territories, many of which are islands. For each island, or island group, we have collaboratively developed lists of invasive non-native species predicted to be a priority because of their high probability of arrival, establishment and subsequent impacts on biodiversity and ecosystems, human health or economies. We have demonstrated the critical importance of cross-boundary collaborations to ensure knowledge on invasive non-native species is shared between regions, and to advance understanding and enable successful implementation of strategies, such as pathway action planning, to manage invasive non-native species. In this talk I will provide insights into the outcomes of the horizon scanning including the importance of collaborations and effective engagement. The networks established and advances in understanding achieved through collaborative research such as this have benefits for people, science and nature.

Keywords: citizen science, ecosystems, Horizon scanning, impact, prioritisation

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The "French Connection": lessons learned from the management of invasive plants in French Overseas Tropical Island Territories

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The French Overseas Territories comprise 11 tropical islands or archipelagoes located in three different oceans (Atlantic, Indian and Pacific), ranging from small atolls to high volcanic islands and from oceanic to semi-continental islands, located within the boundaries of 5 of the 36 global biodiversity hotspots. Their unique and speciose flora (with a total of more than 3,340 endemic vascular plants) is highly threatened by direct and indirect anthropogenic impacts, including alien plant invasions. A total of nearly 300 plant species invading natural and semi-natural ecosystems (excluding weeds in agrosystems) are currently documented from these island territories, with about 30% of them found in 3 territories or more. They include the small tree *Leucaena leucocephala* (in 8 island territories), the water hyacinth *Eichhornia crassipes* (in 6 of them), the succulent herb *Kalanchoe pinnata*, the erect subshrub *Furcraea foetida*, the thorny shrub *Lantana camara* and the tree *Syzygium jambos* (in 5), and the African tulip tree *Spathodea campanulata* (4). Other dominant invaders, such as the strawberry guava *Psidium cattleyanum* (3), the melastomes *Clidemia hirta* and *Miconia calvescens* (3) and the large erect herb *Hedychium gardnerianum* (1) are particularly invasive in rainforests and montane cloud forests. Since 2005, The French Overseas Invasive Alien Species Initiative (" Initiative sur les Espèces Exotiques Envahissantes en Outre-Mer ") of the IUCN French Committee, allowed the creation of a network of local experts, the publication of invasive species management guides, and a dedicated website. Management efforts have greatly benefited from experiences and lessons learned in the different island territories. As an example, well-tested strategies and methods are used to control the small tree *Miconia calvescens* (Melastomataceae) introduced in the 30's in French Polynesia, the 60's in New Caledonia, and the 80's in Martinique. Regional collaborations with other neighboring tropical islands (e.g. Comoros, Mauritius and Seychelles in the Indian Ocean, Fiji and Hawai'i in the Pacific, the Caribbean Islands in the Atlantic) are also important, as they share the same insular challenges. In particular, it could help to prevent further invasions by using common risk assessment, early detection and rapid response systems.

Keywords: invasive plants, management strategies, control methods, network, Miconia

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Invasive species management in the French Southern and Antarctic Lands (TAAF) : past efforts and future challenges

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Alike most islands in the world, the history of animal and plant introductions in the French Southern and Antarctic Lands (TAAF) – formed by Terre Adélie (Antarctic) and a collection of islands lying from tropics (Eparses Islands) to subantarctic (Kerguelen, Crozet, Saint Paul and Amsterdam) in the south western Indian ocean - is strongly correlated with the history of human occupation. Since the beginning of research development in the TAAF, numerous scientific programs have allowed to better document impacts of these non-native species on ecosystems and native biodiversity (e.g. competition, predation, browsing, soil erosion, 'invasional meltdown', transmission of pathogens) but also to understand their distribution and their population dynamics. We will first review this significant work that was used to support the implementation of the first management measures. Beyond early experimental eradication operations carried out in the 1950s, the implementation of a first strategy for the management of invasive alien species has been initiated for almost twenty years to ensure the long-term preservation of the native biodiversity of the islands. This strategy is based on three pillars: prevention of introductions, early detection and eradication/control of invasive populations. We will present here some case studies of the first eradication efforts and impacts on species and ecosystem recovery. Despite initial limited financial and human resources, a total of 7 species of introduced mammals established on 13 islands have already been eradicated and more than 70 invasive plant species have been targeted. Management operations were conducted on islands ranging from 80 hectares to 3,405 hectares. From now on, TAAF are looking to set up a new adapted strategy to meet future challenges on a larger scale (i.e. routine implementation of eradications on islands larger than 1,000 hectares). Perspectives in terms of capacity building, regional networking and fundraising will be presented.

Keywords: invasive species, ecological restoration, protected area, management, biosecurity

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Past, present and future of invasive alien species on the Macaronesian islands

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The European Macaronesian archipelagos (Azores, the Canary Islands, Madeira and Selvagens Islands) are one of the most important biodiversity hotspots in Europe. Biogeographically similar but administratively managed by two countries (Portugal and Spain), these archipelagos suffer common problems posed by biological invasions. We reviewed past and present invasive alien species (IAS) actions carried out in each archipelago in aspects such as : i) building awareness and support, ii) collecting, managing and sharing information, iii) strengthening national policy, legal and institutional frameworks, iv) regional co-operation, v) prevention, vi) early detection and rapid responses, vii) mitigation of impacts, and viii) restoration of native biodiversity. State-of-the-art analysis has allowed the identification of existing gaps and aspects to which more efforts have been allocated. In general, despite some past efforts, vigorous information and education programmes for different target audiences are lacking, and IAS are not formally incorporated to education programmes. Species inventories and exchange of information are insufficient and regional and national law should be still strengthened. Specific aims and prescription regulated by the EU Regulation 1143/2014 for the outermost regions have been timidly (or have not been yet) implemented. Conflicts between the national and EU level have affected the implementaion of IAS legal measures, being urgent to get consistency and harmonisation between policies and legislations. Regional cooperation is scarce, as well as it is among different institutions within some archipelagos. In general, mitigation of impacts has monopolized most of the funds allocated to IAS in all the archipelagos. A considerable much less effort aimed at prevention or early warning actions have been accomplished in the region, despite these being the ones producing the most profitable outputs. Finally, restoration actions related to IAS management are scarce and should be promoted more intensively. Bearing in mind that Macaronesia hosts a tremendous portion of European biodiversity in relation to the area it occupies, it is urgent to implement regional, national and European strategies that quickly have an impact on effectively managing IAS within a region whose vulnerable and fragile ecosystems are still highly threatened.

Keywords: invasive alien species, islands, Macaronesia, review

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Island Biogeography, macroecology, evolution and conservation of marine organisms (Symp.)

Contents

Marine island biogeography: an overview of patterns and mechanisms involved in endemism and community assembly

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In contrast to terrestrial species, marine species have received little attention in studies of island theory. However, in recent years, studies concerning the biogeography, macroecology, and evolution of marine organisms living in islands gained momentum. I will show recent results that highlight the different processes ruling marine versus terrestrial biodiversity, mainly due to major differences in species mobility and colonization potential. I will present advances on theoretical ideas and real data examples to demonstrate: 1) the effects of sea-level dynamics on speciation processes on islands and seamounts, 2) global patterns of paleo and neo-endemism, and 3) archipelagos as functional islands for marine organisms - with focus on Cape Verde Archipelago. I will also bring functional and phylogenetic perspectives (i.e. the effects of environmental filtering, competitive exclusion or neutral mechanisms) on community assembly and endemism of marine island biotas, thus giving context to the other talks of the symposium.

Keywords: functional traits, oceanic islands, marine organisms, speciation, sea, level

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[*] Speaker

Evolution and biogeography of marine organisms on seamounts and oceanic islands

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Islands are natural laboratories for evolution and biogeography studies. From MacArthur and Wilson to present days, understanding processes such as dispersion, extinction, speciation and immigration is key to elucidate currents patterns of islands biogeography. However, these processes have been better investigated for terrestrial/aerial than for marine organisms, for which oceanographic features (*e.g.*, currents, tides) and marine geologic processes (*e.g.*, bioconstruction) limit the analogy between these two realms. Thus, we aimed to review the Island Biogeography Theory in light of marine organisms, to test how species evolutionary history fits theory. We analyzed the evolutionary history of reef fishes that are endemic to Vitória–Trindade Chain (VTC), in the south Atlantic Ocean, to understand their relations to island evolution and sea-level fluctuations. We found that most endemic species, intertidal and cryptobenthic reef fishes, have evolved recently, during recurrent sea-level changes of the Pleistocene epoch where repeated aerial exposure of seamounts provides intermittent connectivity. The pattern is consistent with an ephemeral ecological speciation process. The speciation rate for marine organisms on islands is negatively correlated with immigration rate, similar to findings for terrestrial biodiversity. However, dispersion process is easier for marine species than for terrestrial ones, most niches are filled by immigration and speciation increases with the random accumulation of species with low dispersal ability, with few opportunities for in situ cladogenesis and adaptive radiation. Overall, as the geological history of islands proceeds, they loose terrestrial area by erosion but gain marine area trought deposition of eroded material and bioconstruction. This process could represent more spaces for niche accommodation. Thus, marine speciation rates in oceanic islands seem to increase not only with isolation but also over time. Moreover, we confirm that sea-level fluctuations and seamount presence play critical roles in marine evolution, mainly by intermittent providing connection (*i.e.*, stepping-stones process) for island colonization.

Keywords: endemism, Pleistocene, reef fish, sea level fluctuations, speciation

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*Speaker

Reef fish endemism and functional diversity in oceanic islands

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Factors affecting species composition on islands have been the subject of considerable research, resulting in a broad understanding of assembly patterns in terrestrial communities. Conversely, our understanding of the factors that shape the diversity of marine organisms in islands is still scarce. This lack of knowledge is more evident when we try to infer on processes promoting speciation since marine populations remain highly connected due to its planktonic dispersion. In this sense, endemic species are fundamental study cases/ units to unravel and interpret the ecological and evolutionary processes shaping the structure of marine communities on islands. Using a dataset derived from reef fish checklists for 75 tropical oceanic islands distributed across six marine biogeographic regions, we first evaluated the relative role of historical, biogeographical and environmental factors in shaping reef fish endemism patterns. We then quantified how functional diversity and functional originality differed between endemic and non-endemic species pools. We found that the proportion of endemic species is influenced mainly by biogeographic (e.g., isolation, area) and historical factors (e.g., island age, distance from Quaternary refugia, past coral area). The proportion of endemic species was indeed found to be higher in islands that were more distant from Quaternary refugia and in regions with low species richness, such as the Eastern Pacific and Eastern Atlantic. This is possibly an outcome of the low connectivity between these islands and past refuges during the Quaternary climatic oscillations, which may have prevented the re-colonization of species after extinction events. We also found that non-endemic species have greater functional richness when compared to endemic species, while endemics have greater functional originality. Island endemics and non-endemics were also found to differ in their life-history traits: endemic species are mainly smaller, whereas non-endemics occupy all body size classes. These results provide new insights into the patterns and processes relative to reef fish endemism and functional diversity in oceanic islands.

Keywords: island biogeography, functional originality, life, history traits, environmental filtering, historical factors

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The rise of politics-based marine conservation in oceanic islands

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Every marine conservation biologist is familiar with the term "science-based conservation", which applies to processes where conservation management actions and policy making are driven by scientific evidence. For example, the scientific way to determine the best place and shape for a marine protected area often involves conducting detailed biodiversity surveys and identifying critical habitat, such as nurseries, spawning areas, and migration corridors. On the opposite side of the spectrum is "politics-based conservation": the process by which conservation policy making is entirely driven by conflict avoidance. In this case, the decisions about where to place a marine protected area or how big it should be always starts by excluding areas that are heavily used by fishers, the oil and gas industry, tourists, etc, thus avoiding conflict. Here I will show that, contrarily to what is always portrayed by the media, every large marine protected area created over the past 10 years has followed a politics-based rather than a science-based approach. These MPAs are often centered around oceanic islands and don't include coastal protection, but rather, only open-ocean protection, and are being used to meet arbitrary international targets for conservation. Therefore, they remove the pressure for any further conservation measures without actually protecting anything, and their creation has the potential to do more harm than good to biodiversity in the long run.

Keywords: marine protected areas, Aichi targets

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[*] Speaker

Marine lakes: A view of what is possible in marine islands

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Marine lakes are bodies of seawater entirely surrounded by land. Physically, they fit the definition of habitat islands and, syntactically, they are a simple transposition from the definition of true islands. To what extent might these superficial similarities actually indicate shared biogeographic processes? And to what degree could any shared processes lead to ecological and evolutionary patterns in marine inhabitants of islands that we have long considered hallmarks of terrestrial taxa inhabiting islands? Here, I summarize our ongoing research in marine lakes of the Indo-West Pacific to explore these topics. I draw upon work conducted at scales from tens-of-meters to thousands-of-kilometers across three archipelagos, and from days to decades up to decamillenia, including representatives of most common marine phyla, to examine patterns within and among populations, communities, and species. We find evidence of a great variety of patterns: isolation and eurymixis, stasis and rapid evolution, convergence and divergence, neutral and non-neutral. Some of these are reminiscent of patterns familiar in coastal and open oceans, others are reminiscent of island biogeography and island evolution. I infer these patterns include the results of different balances of drift, gene flow, and selection that are influenced by interactions between the geographic setting, environment, and biology of species. Albeit emerging evidence, these findings raise the prospect of a continuum of process and pattern integrating marine with terrestrial perspectives, both of which may be enriched by the other. Marine island biogeography is in its infancy; it may present situations that are uncommon in the existing literature, but not rare in nature, and thus contribute substantially to a new dynamic outlook on a half century-old theme. Better understanding of the level of overlap of marine and terrestrial island and island-like systems will be facilitated by three advances: (1) development of many descriptive marine studies to reduce the current deficit, (2) design of rigorous comparative studies within and across realms, and (3) modification of conceptual models to accommodate seemingly disparate situations.

Keywords: community ecology, environment, marine, phylogeography, speciation

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Fish as indicators of biodiversity change in coral reefs of the Indian Ocean

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”Fish abundance and diversity” is one of ten Essential Biodiversity Variables (EBVs) used for global ocean assessments, recognizing their importance in trophic pathways in all marine systems. Selecting EBVs for coral reef ecosystems is challenging because of their high inherent variation, particularly for fishes. Here we measured the species diversity, density and size of fish species at reefs in Comoros, Madagascar, Mozambique, Tanzania and Chagos, together with 16 bio-physical variables for each site, to develop a model that tests the sensitivity of reef fish indicators and hence their potential as coral reef EBVs. The analytical approach used space rather than time to represent the wide range of reef conditions across the western Indian Ocean. We first modelled diversity, density and biomass of fish species to determine which bio-physical variables were significant in determining fish assemblages. Geographic location and reef geomorphology were the most significant drivers, explaining 32% of the observed variation in densities and biomass. Species richness also varied geographically with Comoros being the least diverse. Fishing effects only became significant, explaining 6% of variation in biomass when data were analysed at smaller spatial scales. Only in Chagos, with zero fishing pressure and relatively homogeneous geomorphology, did live coral cover correlate with fish assemblage structure. The second analysis used PCA to try to condense key benthic variables and found benthic attributes delineated clearly across two primary PCA axes (48% of total variation): i) from high turf algal cover to exposed sites with high CCA cover; ii) from high coral cover and rugosity to high fleshy algal cover and rubble. This provides a matrix for preliminary modelling which is now testing how responsive are different aggregate fish indicators to variation in environmental conditions and anthropogenic pressures. This paper shows that different geographic / morphological reef systems support different fish assemblages. The broad spatial approach enabled a wide range of benthic variables to be simplifed into two values per site and provides the basis for testing commonly used aggregate fish indicators. These results can contribute to the development of global fish EBVs and to biodiversity targets set by the CBD.

Keywords: indicators, reef fishes, monitoring, essential biodiversity variables (EBVs)

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Temporal patterns of reef fish communities in South Atlantic oceanic islands

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Worldwide marine systems have clear records of intensive human exploration causing serious habitat degradation with consequently high rates of ecosystem functional loss. In this scenario, oceanic islands via their isolation and comparative less anthropogenic influence emerge as landmarks of what we can call as the last marine pristine areas. On the other hand, studies on the terrestrial realm of oceanic islands were the baseline for the understanding of the bioinvasion science, providing iconic examples of plant and animal extinction. However, the marine science in oceanic islands is poorly developed, with few examples from the intertidal and much less from the subtidal. As islands sustain small subsets of the regional biodiversity, with high rates of endemism and expected low functional redundancy among species, the vulnerability of extinction caused by human impacts is comparatively higher. Temporal data from long-term ecological research help us better understand marine organisms in islands (i.e. community assembly over time), as well as their conservation. We will show temporal trends of reef fish abundance and richness from four Brazilian oceanic islands, which vary in isolation, area and human influence. Our methods include seven years of visual census to estimate abundance and biomass of reef fishes. Protection and human use as usual are the main variables explaining change in abundance through time of large species of groupers and parrotfishes. Modelling temporal trajectories of community descriptors showed that some trophic groups were influenced by variations in temperature and primary productivity along the years. The understanding of marine community dynamics as well as management strategies are highly dependent on long term monitoring programs.

Keywords: Brazilian oceanic islands, functional redundancy, long term ecological research, trophic groups

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*Speaker

Island palaeontology (Symp.)

Contents

Island life before Man

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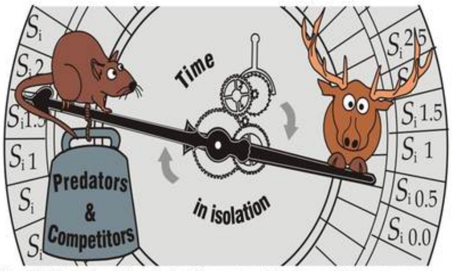
Island biodiversity is changing locally and globally, but at present we have insufficient knowledge of time-series data to assess the degree, nature and consequences of these changes. Nearly all our knowledge on insular biodiversity patterns is derived from studies of extant faunas, which are partly artefacts of ancient colonisations by humans and their commensals. The fossil record provides the necessary baseline to detect and evaluate change and test hypotheses. We tested three models of island biogeography theory: the island rule of body size evolution, the species-area relationship (SAR) and the species-isolation relationship (SIR). We assembled data on body mass and island characteristics, including time, for over 1800 populations of non-volant mammals (including 63 fossil endemic species and 56 introduced species) across 285 islands. We further compiled the number of mammalian species for 36 oceanic islands at colonisation, after speciation and after human arrival to assess the impact of speciation and humans on the native assemblages. The island rule is indeed a pervasive pattern in mammals, exhibited across a broad span of geographical regions, time periods and for introduced as well as native populations. Body size shifts are much more pronounced for populations with greater residence times on the islands. Body size of insular populations is negatively correlated with number of co-occurring mammalian species, confirming an ecological hypothesis of the island rule. We also found that biodiversity patterns for founder populations were consistent with both SAR and SIR, with biodiversity increasing with area and decreasing with isolation. However, resulting biodiversity, that is, after speciation took place, were anomalous, with steep log-log slopes of SAR, and no sign of SIR. Further, anthropogenic introductions have inflated species richness on many islands far above that predicted by SAR theories. We argue that models of island biogeography should include the effects of five processes: immigration, extinction, speciation, time and the impact of human activities.

Keywords: Pleistocene, mammals, fossil record, species, area relationship, island rule



Simplified illustration of the effects of time and predator / competitor pressure on body mass evolution in insular mammals. S_i (size index): body size relative to that of the mainland ancestor. Courtesy: George Lyras.

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[*] Speaker

Pleistocene-Holocene environmental changes on Madagascar and associated extinctions

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On the basis of the late Pleistocene-Holocene fossil record, Madagascar underwent important climatological changes, which in turn had a dramatic impact on the island's ecosystems and the different organisms they held. These vicissitudes led to the extinction or range contraction of a considerable number of endemic land vertebrates. Subsequently, people colonized the island, further extenuating ecological shifts, which resulted in further extinctions. The main objective is to better understand the processes that led to environmental change in the late Pleistocene-Holocene. Over the past decade, new palaeontological and archeological sites have been excavated and studies including, for example, inference from stable isotopes to speleothem analyses have been conducted, which provide new refinement on the impacts of these different events and causes on the island's ecosystems. Further, the date of initial human colonization has been pushed back several millennia and there is good evidence of a Neolithic culture. In the context of this presentation, a synthesis is presented of these different lines of evidence, which in turn provide new insights into the question as to what happened, the time-scale, and separating natural climatic change versus human-induced.

Keywords: Madagascar, late Pleistocene, Holocene, natural change, human induced change

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Quaternary extinction of large rainforest herbivores on Indonesia's largest island, Sumatra

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Sumatra is the world's sixth largest island, and Indonesia's largest. It hosts 201 mammal species, of which nine are endemic to mainland Sumatra, fourteen to Mentawai islands, and 22 found nowhere else in Indonesia. Unlike other major islands in Southeast Asia, it records very few Quaternary extinctions. Here, we report the first globally extinct taxon from the island. *Hexaprotodon,* the Asian hippo, is represented by the anterior portion of a second lower molar as well as some canine fragments. These were recovered from Ngalau Gupin, a cave site in the Padang Highlands. A tapir molar from the same site has been dated to at least 45,000 years old by uranium series dating. Other than the hippo, the banteng, the buffalo, and the Javan rhino became extirpated from the island, probably sometime in the historical period. Examination of carbon and oxygen isotope values from fossil and modern large mammal communities show no significant differences in either isotope (Mann-Whitney U: carbon U=1666, p=0.1704; oxygen U=1855, p=0.759). This suggests there have been no significant ecological shifts over the Pleistocene at the resolution of these proxies. Unlike other Quaternary extinction events on islands, the largest herbivore on the island is still extant, suggesting that anthropogenic overkill alone is unlikely to be responsible. We suggest that an interplay between decreased carrying capacity, increased hunting, and separation from Southeast Asian source populations may have adversely affected the large, but not medium or very large, herbivores on this island.

Keywords: Padang highlands, Asian hippo, fossil, palaeontology, megafauna

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[*] Speaker

Early colonisation of the Philippine islands

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Past dispersal patterns of terrestrial vertebrates towards and within the Philippine archipelago remain a widely debated topic. As none of these islands has ever been connected to mainland Southeast Asia, even during the most severe quaternary sea level drops, the question of ancient island hopping is still controversial. A West-East main flow from Borneo via Palawan Island seems preferred by scholars nowadays while older studies were favoring a North-South way from China via Taiwa – this latter island being connected to the continent during some glacial periods while the whole Philippines were not. An almost complete skeleton of the controversial "*Rhinoceros philippinensis* von Koenigswald, 1956" was recently discovered at Kalinga site (Northern Luzon) from a 709±68 kya archeological layer along with butchery marks and lithic artefacts. This early Middle Pleistocene individual considerably adds to the knowledge of the Philippine rhinocerotid species. The completeness of the specimen further allows us to test the different phylogenetic and subsequently paleobiogeographic scenarios at hand. 309 cranio-mandibular, dental, and postcranial characters robustly support the unsuspected existence of a Southeast Asian Pleistocene clade, including the Philippine rhino. It is closely related to the Sumatran rhino + *Rhinoceros* clade and groups *Rhinoceros fusuiensis* from Asian mainland and *Rhinoceros hayasakai* from Taiwan. Our phylogenetic results strongly suggest an island-hopping dispersal hypothesis for this clade, from China toward Luzon via Taiwan by early Pleistocene times. The phylogenetically-constrained reconstructed body mass and gracility of the new rhino genus clearly points to a tendency to dwarfism from the continental species present in China, through the continental island species on Taiwan and until the oceanic island species in the Philippines. This rhino is the first perissodactyl supporting the island rule hypothesis, with body weight and limb bone robustness significantly decreasing from Asian mainland to Luzon.

Keywords: Rhino, Kalinga, early middle Pleistocene

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Island reptiles: the rich diversity of continental and oceanic islands (Symp.)

Contents

Biogeography of Gulf of Guinea Oceanic Island Reptiles

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Studies on the reptile fauna of the oceanic islands of the Gulf of Guinea had its initial impetus during the second half of the nineteenth century leading to the description of several new forms and the overall cataloguing of the occurring group of species. After this period, studies on the taxonomy and biogeography of this fauna in the region came to an almost complete halt. Since the early 2000's, backed with molecular data, the reptile fauna of these islands started to be investigated, leading to the discovery and description of five new endemic species and several subspecies. Evidence shows that species diversity is even higher that currently documented on these islands, and additional work will reveal new species. These new discoveries have increased the percentage of endemic reptiles and contributed to a new paradigm on the biogeographic and evolutionary patterns for these islands. Similar to other taxonomic groups (e.g. mammals and amphibians) our data on reptiles shows several modes of post-colonization diversification on these islands – 1) single representatives of certain genera arrived at specific islands and speciated *in situ*; 2) sister-taxa occurring on two or more islands diversified through island-hoping colonization; 3) independent colonization of different islands by representatives of the same genus; and 4) populations diversified after sea-level changes fragmented some of the islands. Besides the endemics, at least three species represent recent introductions, possibly through anthropogenic mediated dispersal. Biogeographically, the reptile fauna of the Gulf of Guinea Oceanic Islands is composed by Western and Central African Groups, but there are noticeable differences between islands, with the southern islands having representatives of southern and eastern African clades. Our current knowledge of reptile diversity in these islands raises several hypotheses that need to be formally addressed and that will likely contribute to a better understanding of the biogeography, colonization and diversification processes in oceanic islands.

Keywords: Reptilia, Africa, new species, diversification, endemism

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*Speaker

Biodiversity growth on the volcanic ocean islands and the roles of in situ cladogenesis and immigration: case with the reptiles

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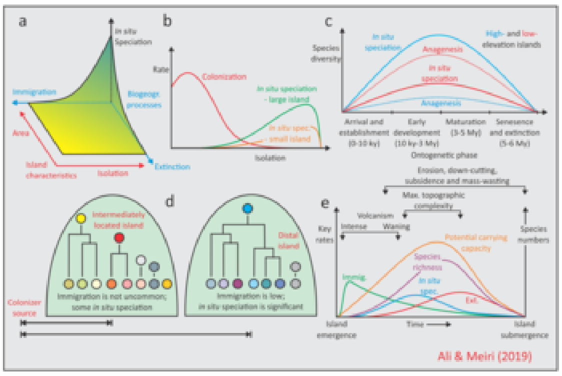

Ali & Meiri (2019)

Figure 1. Most models explaining the growth of biodiversity on oceanic islands assume that *in situ* cladogenesis is a key contributor: (a) Lomolino (2000); (b) Heaney (2000); (c) Stuessy (2007); (d) Emerson and Gillespie (2008); (e) Borregaard et al. (2016). For each, note the role of cladogensis ('*in situ* speciation' or 'phylogenesis').

Theoretical models explaining biodiversity growth on the volcanic oceanic islands assume that in situ cladogenesis is a major contributor. To evaluate this proposition, we examined the extent to which the process, rather than immigration and within-archipelago anagenesis, shapes reptile diversity on the volcanic oceans islands (the animals belonging to this group are particularly well suited for carrying out such a test). Occurrence data were compiled for the 194 terrestrial reptile species occupying 53 volcanically-constructed middle- to low-latitude landmasses worldwide. These included forms on 'model' archipelagos for evolution such as the Galapagos, Lesser Antilles, Canaries, Comoros, and the Mascarenes. Using phylogenetic data, we deduced which species resulted from in situ cladogenesis. Statistical models were then used to establish whether an island's area, age, maximum altitude, or isolation influenced the process. We also assessed whether the presence on a landmass of a non-sister congener exerted a control. Despite 273 native island-species records, there are only 8–12 cases of the phenomenon, including just two radiations. Diversification frequencies are uncorrelated with island area, age, maximum altitude, and isolation. Furthermore, there is no indication that the co-occurrence of non-sister congeners stymies the process. We therefore contend that in situ cladogenesis plays only a minor role in the accumulation of reptile diversity on individual oceanic islands; growth results primarily from immigration and between islands movements followed by anagenesis. This, however, is not a simple matter. Clusters that are far or challenging to get to have relatively few clades (3–8), some of which have many species (6–14), and all host at least one endemic genus. In these settings, diversity grows mainly by intra-archipelago transfer followed by within-island anagenetic speciation. In contrast, those island groups that are characterized by short distances and conducive transit conditions have been settled by many ancestor-colonizers (≥ 14), but each clade has few derived species (≤ 4). These archipelagoes lack especially distinctive lineages. Models explaining the assembly and growth of terrestrial biotic suites on the volcanic ocean islands thus need to accommodate these new insights.

Keywords: cladogenesis, island biogeography, biodiversity accumulation, reptiles, terrestrial vertebrates

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*Speaker

Ecological and evolutionary determinism in Greater Antillean reptiles

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Some of the most important insights into the ecological and evolutionary processes of diversification and speciation have come from studies of island adaptive radiations, yet relatively few studies have examined how these radiations initiate. We suggest that *Anolis sagrei* (Brown Anoles) is a candidate for understanding the origins of the Caribbean *Anolis* adaptive radiation and propose that detailed investigation of the morphological and genetic variation of this widespread species can help to provide considerable insight into how a colonizing anole species begins to undergo allopatric diversification, phenotypic divergence, and, potentially, speciation. To investigate the extent of diversification across *A. sagrei*, the most widespread species of anoles, we undertook a genetic and morphological analysis of representative populations across the entire native range of the species, encompassing 295 individuals from 95 locations. We find that at the broadest scale, populations colonizing areas with fewer closely related competitors tend to evolve larger body size and larger number of toepads, on average. Such a trend follows expectations for an ecological release scenario, whereby populations freed from competition with close relatives evolve towards different morphological and ecological optima. Further, colonization of islands can dramatically influence the evolutionary trajectories of organisms, with both deterministic and stochastic processes driving adaptation and diversification. Some island colonists evolve extremely large or small body sizes, presumably in response to unique ecological circumstances present on islands. One example of this phenomenon, the West Indian boas, includes both small ($<$ 90cm) and large (4m) species occurring on the Greater Antilles and Bahamas Platform, with some islands supporting pairs or trios of body-size divergent species. Here we show that small body size evolved repeatedly on separate islands in association with specialization in substrate use. Our results further suggest that microhabitat specialization is linked to increased rates of head shape diversification among specialists. Our findings show that ecological specialization following island colonization promotes morphological diversity through deterministic body size evolution and cranial morphological diversification that is contingent on island- and species-specific factors.

Keywords: Anolis, boas, Caribbean, determinism, reptiles

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The evolution of an island phenotype: results from an experimental introduction

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Island lizards are often characterized by differences in morphology compared to their mainland counterparts. Although previous studies have documented differences in body size, head morphology, bite force and diet in insular environments, the selective pressures driving the evolution of this insular phenotype remain poorly known. Moreover, how fast lizards evolve these insular phenotypes has never been assessed. Here we provide data for *Podarcis* lizards in insular ecosystems of Croatia and Greece documenting the possible drivers of the observed phenotypic differences in insular lizards. Additionally, we provide data from a replicated introduction experiment addressing the issue of how fast these phenotypes evolve. Our results show that drivers of phenotypic variation are related to island size, food availability, population density as well as founder effects. Our results of the replicated introduction experiment show that these changes occur much faster than what is typically thought and suggest an important role for phenotypic plasticity as the initial response to changes in environmental conditions when confronted with island environments.

Keywords: lizards, diet, bite force, morphology, insularity, plasticity

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Lizard discoveries and rediscoveries in the New Caledonian region

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Despite more than 150 years of herpetological research in New Caledonia, including 40 years of fine-scale sampling across the territory as a whole, novelties continue to be found that shed light on evolutionary patterns and processes in the southwest Pacific. The most noteworthy of these is the discovery of a new genus and species of giant gecko with semi-aquatic habits. It is not closely related to the other giant geckos (*Rhacodactylus*, *Mniarogekko*, and *Correlophus*), but rather is sister to *Dierogekko*, the smallest-bodied genus in the region. Morphologically, however, it resembles species of the New Zealand genus *Dactylocnemis*, one over very few other geckos globally to exhibit any aquatic tendencies. It also shares some features with the extinct *Hoplodactylus delcourti*, the largest gecko that ever lived. This species had been presumed to have a New Zealand origin, but recent ancient DNA study has revealed that it is also part of the New Caledonian radiation. Among eugongylid skinks another giant species, *Phoboscincus bocourti*, has been rediscovered on several islands in the Île des Pins region. Preliminary data suggest that this species has highly restricted ecological preferences and occurs in very small populations that are particularly susceptible to habitat degradation and introduced mammals. Another skink, *Epibator greeri*, previously known from two specimens from near Koumac in the north of the island, has been rediscovered in the southern Grande Terre, 265 km distant. Its congener, *E. insularis*, was described in early 2019 from Île Walpole, 140 km distant from both the Île des Pins and the Loyalty Islands, and is the first endemic terrestrial vertebrate recorded from the island. These and other recent discoveries indicate that 1) current estimates of lizard species richness and endemism are underestimated, 2) there have been multiple *in situ* derivations of large body size in New Caledonian geckos, 3) some geckos and skinks exhibit unique ecologies that have helped conceal their existence or persistence, and 4) small, low-lying satellite islands play a role in both the generation and the conservation of lizard species in the New Caledonian region.

Keywords: Reptilia, gigantism, endemism, gecko, skink

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Island rewilding with giant tortoises: state of the art and future directions (Symp.)

Contents

Wild and rewilded: Giant Aldabra tortoises in the Western Indian Ocean

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Giant tortoises were widespread on islands around the world until humans recently arrived and drove almost all of them to extinction. Seven out of eight endemic WIO species have gone extinct, with many negative effects for the islands' remaining native biodiversity, as the giant tortoises were key ecosystem engineers. What could be a picture of despair has been turned into a conservation and restoration success, as the WIO in the last two decades has emerged as a world-leading region in the development and application of rewilding as a conservation action. An ever-increasing number of rewilding projects throughout the WIO aim to resurrect the megafaunal ecosystem functions of the extinct giant tortoises by rewilding with the sole surviving WIO species, the Aldabra giant tortoise (*Aldabrachelys gigantea*), which survives in the wild on Aldabra Atoll, Seychelles. The tortoises currently do well on the atoll, with a current population of about 100,000. Unfortunately, their ecosystem is threatened by climate change. Drought is already a serious issue and sea level rise is poised to drown large areas of the atoll in the next few hundred years. I argue that conservation management of both wild and rewilded tortoises and their respective ecosystems can learn a lot from each other, especially from a closer long-term integration of research activities on Aldabra and rewilding projects in the WIO. There are still major gaps in our basic understanding of tortoise biology, ecology, and genetics. Joint focused research in these areas would provide a solid understanding with which to optimize the management of tortoise-mediated ecosystem functioning in rewilding sites, and minimise the impacts of projected climate change on giant tortoises and their ecosystem functions on Aldabra. Lastly, one aspect that is often forgotten in tortoise rewilding research is how intimately giant tortoises are linked to the WIO nations' local cultures, and how closely many rewilding projects are linked to their socio-economic systems. Promoting the use of the Aldabra giant tortoise as an icon for the WIO to encourage regional co-operation is a low-hanging fruit waiting to be picked and dispersed.

Keywords: Aldabra giant tortoise, ecosystem restoration, Giant tortoise, rewilding

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*Speaker

Pleistocene Rewilding of the Bahama Islands

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Rewilding is the restoration of extinct species - or their ecological surrogates – to their former habitats. Not only does rewilding restore species (or their surrogates) to their former range, but it restores the ecosystemic services of those species. In the Bahamas examples have been the introduction of hutias (*Geocapromys ingrahami*) to the Exuma Cays and the release of confiscated (and therefore possibly disease-infested) rock iguanas (*Cyclura rileyi*) to cays off of San Salvador. The hutias dramatically transformed the vegetation of their new habitats, likely because of the absence of an extinct predator, *Tyto pollens.* The iguana transfer was conducted for epidemiological reasons; rewilding was the byproduct. Extant relatives of extinct Pleistocene species have the potential to be rewilded in the Bahamas. Examples are the Isabela Island giant tortoise (*Chelonidis vicina*), which is the closest living relative to the extinct Bahamian tortoise *Chelonoidis alburyornum*; the Cuban crocodile (*Crocodylus rhombifer*), which the historical and fossil record shows to have been widespread throughout the Bahamas; and the Hawaiian monk seal (*Neomonachus schauinslandi*), which would be an ecological surrogate for the extinct West Indian monk seal (*N. tropicalis*), last seen in the mid-Twentieth Century. There are controversies, risks and virtues attendant to the rewilding of these species.

Keywords: rewilding, extinct species, ecological surrogates, Cuban crocodile, monk seal, extinct Bahamian tortoise

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*Speaker

The world's largest rewilded tortoise herd and its island ecosystem: The Frégate Island experience

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Megaherbivore reintroductions are high in risk and uncertainty. Environmental managers are expected to mitigate against these through scientific research, and adaptive management of project goals and expectations. Often, ecosystems requiring restoration are on private land with established human activities. I present how an initially small reintroduction project with Aldabra giant tortoises (Aldabrachelys gigantea) on Frégate Island, a 220 hectare private eco-resort island in the Seychelles, has grown into the world's largest rewilded tortoise herd. I present and discuss the impact of the tortoises on the island's ecosystem, the challenges that are associated with managing the herd, and how to maximise the impact of the herd in ongoing habitat restoration projects. From a small founder population of 40 individuals, Frégate Island now boasts more than 3500 free roaming Aldabra giant tortoises. This was achieved through habitat restoration, protection from human influence, and additional tortoise reintroductions. The activities of the self-sustaining, free-roaming tortoise herd have created heterogeneous habitats over large areas of the island, creating a wilder ecosystem and reinforcing key ecosystem functions, such as seed dispersal and nutrient cycling, which directly supports a number of endemic Seychelles bird and insect species. However, this key component of rewilding projects, is carried out within the boundaries of balancing business operation requirements. On the island, human influence is limited, but allowing resort guests to interact with the tortoises in a wild ecosystem is providing an excellent opportunity to demonstrate rewilding initiatives and restoration outcomes important for managing stakeholder expectations. On Frégate Island, the rewilded tortoise herd is low-risk, cost effective, with minimal social challenges, although the current high density of the tortoise herd requires active management through translocations to other rewilding projects. These projects benefit from understanding the long-term impacts of island rewilding with tortoises as observed on Frégate Island.

Keywords: conservation, giant tortoise, island, restoration, rewilding

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[*] Speaker

A fire-fighting perspective on rewilding Madagascar with giant tortoises

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Large vertebrates affect fire regimes by consuming plant matter that would otherwise accumulate as fuel. While fire was part of the natural landscape in pre-human Madagascar, today it is of a much higher intensity and frequency due to (1) the loss of the island's megaherbivore community, (2) the persistent and deliberate use of fire by humans, and (3) the creation and propagation of fire-prone grasslands. Madagascar's once diverse vertebrate herbivore assemblage of now-extinct primates, hippos, elephant birds and giant tortoises engineered the landscape. Giant tortoises were particularly important because they could attain high densities, maintain short-cropped grazing lawns and consume vast quantities of dry leaf litter, thereby reducing the fire fuel load and impact of natural fires. Madagascar's remnant and rapidly disappearing forests, home to one of the world's largest and most threatened endemic biota, are threatened by annual uncontrolled wildfires, invariably started to improve pasture for grazing cattle. With supporting evidence from studies of degraded ecosystems in Mauritius and Rodrigues that have been rewilded with Aldabra giant tortoises, we argue that rewilding Madagascar with giant tortoises is a viable landscape-based, long-term, low-maintenance approach to substantially lower the risk and impact of fires on forests at risk of fire in Madagascar. Giant tortoises would not only reduce above-ground plant biomass, but also help restore plant distribution through seed dispersal, and create a mosaic of habitats. Testing this approach as soon as possible is critical, as fire-proneness is projected to increase with climate change in large parts of Madagascar.

Keywords: ecological replacement, Madagascar, restoration, rewilding, tortoises

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Potential Giant tortoise rewilding on La Réunion: restoration of a recently extinct keystone ecosystem engineer

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Until recently (past 175-3000 years) giant land tortoises on remote tropical and sub-tropical islands represented the last remaining relicts of reptile dominated ecosystems. Initial late-human discovery and settlement of island led to rapid extinction of giant tortoises worldwide: a) South Western Pacific (New Caledonia, Fiji, Vanuatu) 2000-3000yrs BP; b) Greater Antilles (Bahamas, Turk-Caicos, Cuba, Hispaniola) 900-4000yrs BP; and Western Indian Ocean (Mascarenes and Madagascar) 175-1000yrs BP. In the Mascarenes Human discovery in the early 16thcentury led to multiple extinctions of several giant tortoise species (endemic genus *Cylindraspis*) by the middle of the 19thcentury. The La Réunion Giant Tortoises (*Cylindraspis indica*) were extirpated by 1840. Yet, after almost two hundred yeas there remains a strong indigenous cultural attachment to tortoises, as evidenced by the importation and widespread husbandry of radiated tortoises (*Astrochelys radiata*) from nearby Madagascar. Recent efforts in the Seychelles to re-introduce the surviving Aldabra Giant tortoise (*Aldabrachelys gigantea*) to other granitic Islands in the Seychelles have been successful and are continuing. In Mauritius rewilding of Aldabra tortoises (as a proxy replacement for the extinct local forms) has proceeded on Round Island, Ile aux Aigrettes and Rodrigues over the past two decades leading to dramatic successes in native ecosystem restoration. Aldabra tortoises are currently being bred in numbers in captivity on La Réunion and are potentially available locally for experimental release (controlled/confined) in native or mixed native/alien ecosystems on the Island. We here evaluate alternative experimental protocols and potential sites for tortoise rewilding on La Réunion. Unlike any other accidental or intentional alien species introductions on Islands, giant tortoise rewilding is completely reversable if unanticipated environmental impacts prove detrimental.

Keywords: La Réunion, proxy species, restoration, rewilding, tortoise

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New insights into the assembly of island biota, filtering effects and disharmony (Symp.)

Contents

Disharmony of the world's island floras

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Disharmony is a key concept in island biology that describes the biased representation of higher taxa on islands compared to their mainland source regions. Although differential colonization success of taxa is predicted by selective dispersal, environmental and biotic filtering, the empirical evidence for disharmony remains largely anecdotal. Here, we develop a novel method for delineating island source regions and present the first global quantitative assessment of island disharmony. We analyzed the overall compositional bias of 320 island floras and examined the over- or under-representation on islands for 450 plant families. We found that the compositional bias of island floras is strongly predicted by geographical and climatic island characteristics (isolation, area, geologic origin, temperature, precipitation), whereas the representation of individual families is only weakly related to family-specific characteristics (family size, family age, taxonomic group, functional traits), indicating that the taxonomic scope of the disharmony concept has historically limited its wider applicability. Our results provide a strong foundation for integrating disharmony with quantitative functional and phylogenetic approaches in order to gain a deeper understanding of assembly processes on islands.

Keywords: source regions, island syndromes, generalized dissimilarity modelling, assembly processes, ancestral area reconstruction

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Drivers of orchid diversity, endemism and disharmony on islands

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The Orchidaceae are highly diverse (≈28,000 species) and have fascinated scientists for over 150 years, owing to their complex biotic interactions and attractive floral morphology. The extraordinary diversity and cosmopolitan distribution of orchids is often attributed to their 'dust-sized' seeds, which are produced in huge quantities and can disperse thousands of kilometers by wind currents. In this regard, orchids are expected to be proficient long-distance dispersers, which has been invoked to explain their sometimes rapid colonisation of volcanic islands or isolated archipelagos. Despite this, recent evidence suggests that patterns of orchid diversity on islands at the global scale are spatially complex, being under-represented on most islands, yet highly diverse on a small number of islands (e.g. in the western Pacific, Caribbean, La Réunion). This finding, however, may actually be an artefact of the analyses, which do not take into account orchid growth form, island type or the spatial arrangement of islands. Here, we present a comprehensive global analysis of orchids on 449 islands, relating patterns of orchid diversity and endemism to geophysical (island area, geographical isolation, age, topographic heterogeneity) and bioclimatic (forest cover, cloud cover, precipitation, temperature) island characteristics using Linear Mixed Effects Models. In contrast to previous studies, we split orchids into two functional growth forms (epiphytic and terrestrial) and determine whether their diversity patterns can be predicted by the same factors. We then compare drivers of total orchid diversity and endemism on islands, making the additional distinction between island types (continental, oceanic, continental fragment). Epiphytic and terrestrial orchids showed variable diversity patterns among islands, both being positively related to increasing units of cloud cover, temperature, and island area, yet responding differently to all other variables. Similarly, determinants of total orchid diversity and endemism varied across different island types, demonstrating a complex interplay of biogeographic and bioclimatic factors. These results illustrate that by considering key functional differences among growth forms, island types, and the spatial arrangement of islands, we can enhance our understanding of species diversity patterns on islands.

Keywords: endemism, disharmony, diversity, growth form, island type, orchids

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*Speaker

Using islands to understand the dynamics of ecological networks: 1st lessons from Hawaii

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Interactions among species remain elusive in efforts to understand and forecast biodiversity dynamics. Towards this end, network-based approaches have the potential to simplify species interactions within a common formal mathematical framework. However, testing the utility of such approaches for understanding how environments are changing, requires simple systems. Islands, especially remote oceanic archipelagos, due to their discrete nature and isolation, coupled with the resulting accumulation of locally endemic species and high turnover in diversity, offer a microcosm for examining biodiversity dynamics with network modeling. Here, we examine ecological interactions of arthropods in the Hawaiian Islands. We use the age structure of the islands as snapshots in time to assess how these interactions change over time. We used quantitative NGS metabarcoding to provide molecular identifiers for diversity estimates (richness, abundance, turnover) in communities of different ages in Hawaii. We couple these data with historical information on species interactions that we are assembling of all known trophic interactions among organisms in Hawaii. Data included information from peer reviewed and grey literature, as well as information from the Hawaii Department of Agriculture and U.S. Geological Survey. We connected historical data with metabarcoding data by building a DNA-barcode reference library that allows each barcode to be connected to a known species. We then analyze the heterogeneity of various bipartite networks by studying their degree distribution and related network properties such as vulnerability (e.g. number of predators or parasitoids) and generality (e.g. number of resources). We find network structure changes according to substrate age and relative to composition of taxa at trophic levels, particularly as to how that composition reflects the number of non-natives. With the model we can make predictions for how interactions change over geological time, and how interactions are likely to change with the onslaught of non-native arrivals, focusing in particular on ecological tipping points.

Keywords: biotic interactions, networks, biodiversity, conservation, metabarcoding

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Functional traits and life history dimensions explain filtering in island communities

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Dominant theories in island biogeography, such as the Equilibrium Theory of Island Biogeography (ETIB) and the General Dynamic Model (GDM), provide conceptual frameworks to quantitatively examine diversity patterns across islands. However, little is known about community assembly processes on islands or the mechanisms shaping it. The composition of island biotas likely reflects the net effect of multiple ecological processes on islands, such as dispersal and environmental filtering, which suggest that island communities assemble non-randomly and not neutrally, as assumed by the ETIB and GDM. Functional traits capture variation in ecological strategies among species and therefore can directly be linked to mechanisms associated with community assembly. However, trait-based frameworks were predominantly developed for mainland communities, and their application to islands remains limited. We developed and tested a trait-based framework to examine community assembly on islands. We used a novel dataset of woody plants on 40 small islands in the Raja Ampat Archipelago in Indonesia and collected functional traits (related to leaf, stem, seed, and whole-plant) that represent major dimensions of variation in plant form and function. When grouping traits into life history dimensions related to species dispersal and environmental adaptations, we found evidence that island communities were jointly shaped by dispersal and environmental filtering and that the relative importance of these processes was affected by island area. Small islands were generally more functionally underdispersed than larger islands, indicating that the filtering strength decreased non-linearly with increasing island area. Small island communities were more strongly shaped by dispersal constraints and limited niche space, whereas greater niche differentiation enhanced functional diversity of communities on larger islands. Our trait-based framework indicated that island communities are shaped by non-random assembly processes that vary with island area independent of species richness, thereby questioning whether neutral based models adequately describe dispersal and establishment dynamics of island floras.

Keywords: Functional biogeography, community assembly, functional dispersion, species composition

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[*] Speaker

The influence of native species composition on the invasibility of island floras across spatial scales

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The establishment of alien species on oceanic islands is thought to be associated with the availability of empty niche space, reflecting abiotic and biotic filtering that generates species-poor, disharmonic native island biotas. Consequently, alien species that are distantly related to and are functionally distinct from native species should be more likely to establish on more remote islands (i.e. Darwin's naturalization hypothesis). Here, we test these hypotheses for flowering plants at two spatial scales. First, at the island scale, we model the number and proportion of naturalized alien plant species per island as a function of socioeconomic factors, biogeographic characteristics of islands, and phylogenetic and compositional properties of their native floras. These properties include a quantitative measure of compositional disharmony, phylogenetic community metrics quantifying the degree of clustering of the native flora, and the mean phylogenetic distance between native and alien species of island assemblages. Our analyses were based on species composition data for a global set of more than 400 islands from the Global Inventory of Floras and Traits database (GIFT; http://gift.uni-goettingen.de) and the Global Naturalized Alien Flora database (GloNAF; http://www.glonaf.org). Second, at the local community scale, we model individual species occurrences of alien and native woody plant species. Using 9,655 forest plots from 101 Pacific islands, we consider the extent to which alien species' traits and their relatedness to native species affect establishment. We expect a positive effect of compositional disharmony and phylogenetic clustering of native island floras on the number and proportion of naturalized alien plant species at the island scale. At the local community scale however, we anticipate an even stronger effect of phylogenetic distance between native and alien species on alien species establishment, because interactions (e.g., competition, facilitation) between alien and native species are likely to be strongest at this scale. Our results shed light on the invasibility of native plant communities on oceanic islands at different spatial scales, and may help to predict island assemblages that are most vulnerable to future invasions and ecological strategies that are associated with future plant invaders.

Keywords: Darwin's naturalization hypothesis, invasions, naturalized species, phylogenetic structure, species composition

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Plant-animal interactions as drivers of biodiversity conservation on islands (Symp.)

Contents

A global review of frugivory and seed dispersal on islands

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Published information on frugivory and seed dispersal on islands is widespread, patchy, and heterogeneous among the topics and islands concerned. A systematic literature search on islands was performed using Internet scientific search engines. To the best of our knowledge, this is the first review carried out at a global scale, covering frugivory and seed dispersal on islands. About 450 contributions were retrieved, with most of the knowledge focused on New Zealand (large area), the Canaries and Puerto Rico, which were the better-studied islands. They were very few studies in Pacific archipelagos near Asia and Australia, and in the Indian Ocean. Most studies were carried out during the present century, especially during the last decade. Island ecosystems are comparatively simple, so they are ideal for developing and testing interesting and original ecological and evolutionary hypotheses. Perhaps, more in-depth studies concerning seed dispersal effectiveness, non-standard mechanisms of dispersal, or complete ecological networks are more feasible on an island setting, and particularly oceanic islands, than in a more complex continental environment. In addition, comparisons among archipelagos offer opportunities for development of general theories. Indeed, the typical low biodiversity, high endemicity, and ecological simplicity of oceanic islands is a most valuable advantage. From a conservation perspective, data from the IUCN, shows that most reported extinctions in the past 500 years have occurred on islands, both for vertebrates and plants. The same pattern is found when considering only those extinctions caused by introduced alien species, one of the greatest threats to the biota of isolated territories. Therefore, it is vital to know both how native systems work and at the same time to evaluate how alien species affect native interaction networks, altering the natural order of interactions. This information is essential to halt biodiversity loss and to guide restoration efforts on islands.

Keywords: conservation, restoration, mutualistic interactions, networks, plant dissemination, seed dispersal

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Double mutualisms: a global island phenomenon

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A double mutualism (DM) occurs when two interacting species benefit each other in two different functions, *e.g.* when an animal species acts both as pollinator and seed disperser of the same plant. Besides the double benefit, a DM also imposes a larger risk to both functions if the performance of one partner declines. We conducted the first global review of DMs involving pollinators and seed dispersers, aiming to: (1) assess their prevalence across ecosystems and biogeographical regions; (2) identify the main plant and animal taxa, and their traits, implicated in DMs; and (3) evaluate the conservation status of double mutualist species. We compiled published and unpublished DM records using specific search terms, noting the species involved, their conservation status and geographic location, as well as the type of study (species vs community-level) in which the DM was detected. We identified 302 DM cases involving 207 plant and 92 animal species from 16 mainland and 17 island areas. Most records come from tropical regions and islands. Animals included birds (62%), mammals (22%), and reptiles (16%), mostly opportunist species; only 18% were nectarivores. Plants were mainly fleshy-fruited shrub or tree species (59%) with actinomorphic flowers that were visited by several or many pollinator species (87%). Most (56%) DMs were detected in community-level studies. DMs are mostly prevalent in ecosystems with limited food resources and mutualist partners, and with high generalization levels. Nearly 30% of the species involved in DMs are threatened according to IUCN criteria, 68% of which are found on islands. The high prevalence of DM on islands paired with the threat status of island species suggest that the loss of a double mutualists and its cascading consequences may have a severe impact on community composition and functioning of fragile island ecosystems.

Keywords: pollination, seed dispersal, mutualism, global patterns

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*Speaker

The forgotten fauna: native seed predators on islands

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Seed predation by alien rodents is frequently seen as a major threat to "naïve" island floras. However, studies examining seed predation by alien rodents on islands only rarely present their findings within the evolutionary and ecological context of historical seed predation by native species. Here, we demonstrate that islands have actually lost many native seed predators-such as parrots and finches-and these would have exerted considerable evolutionary and ecological pressures in insular pre-human ecosystems. Using examples from three iconic island groups-New Zealand, Hawaii, and the Mascarenes-we illustrate how these lost species could have shaped and influenced pre-human environments. We argue that these important interactions must be recognised if we are to truly understand the role of alien seed predators on islands, and whether they are replacing predation pressures once exerted by extinct species, or introducing truly novel seed predation pressures. More broadly, the loss of negative interactions like seed predation receives very little attention compared to the loss of positive interactions such as seed dispersal and pollination mutualisms. However, we argue that negative interactions are an integral part of any ecosystem, and must be acknowledged as such if we are to achieve holistic restoration frameworks for insular ecosystems.

Keywords: plant animal interactions, extinction, seed predation, conservation, invasive species

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Threatened plant seeks pollinator (or when conservation practices prevent mutualistic interactions)

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Island habitats are scenarios where 'rare' plant-animal mutualisms usually occur, and these interactions are key for maintenance of insular flora. However, the importance of mutualistic interactions seems to be overlooked when applying conservation practices. In this talk, we present results on a study about the pollination system of *Lotus maculatus* (Fabaceae), a plant species endemic to Tenerife (Canary Islands) whose pollinators have been unknown (or supposed to be birds) for a long time. This plant has also been object of several plans and actions for its conservation, but unfortunately with no plenty successful results. Here, we present a study on the pollination ecology of this legume that was carried out in both the only natural population and several plantations of *L. maculatus*. After more than 70 hours of direct observation, birds seemed to ignore the plant, whereas insects performed non-legitimate visits to its flowers. In this talk, we show that the Canary lizard *Gallotia galloti* is the most reliable animal for the pollination of these threatened plant. This lizard species not only is its most frequent flower visitor, but also is able to carry pollen grains and promote the fruit production of *L. maculatus*. Lastly, we expose some examples of conservation practices that, far away of helping the plant to recover, have prevented its reproductive success by avoiding almost the unique way for its pollination. Hopefully, increasing our knowledge and understanding of natural history of 'rare' mutualistic interactions on islands will be helpful to apply more efficient conservation practices.

Keywords: conservation practices, endemic lizard, endemic plant, Gallotia galloti, Lotus maculatus, pollination

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*Speaker

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The role of morphological traits in mutualistic interactions among plants and vertebrates in the Galápagos

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Frugivory in lizards is often assumed to be constrained by body size; only large individuals are considered capable of consuming fruits, with the potential of acting as seed dispersers. We studied the entire radiation of lava lizards (*Microlophus* spp.) in the Galapagos to investigate whether frugivory is related to body size and explore the effect of seed ingestion on seedling emergence. Our results showed that fruit consumption was common regardless of body size, and that lizards are important seed dispersers throughout the year and across the whole archipelago. On the other hand, relying on floral morphology to assess pollination systems has been shown to underestimate the ecological service that novel mutualisms can provide. Although vertebrates with opportunistic food habits are common on islands, little is known about how effective they are as pollinators. We thus investigated whether native insectivorous and frugivorous birds act as pollinators by means of pollinator exclusion experiments, and then tested if birds show any preference for specific floral traits. Galápagos passerines are not specialized flower-visitors, either in feeding habits or in terms of morphology, but bird-flower visitation seems to be very common across the entire archipelago. Non-metric multidimensional scaling (NMDS) was used to evaluate the distribution of 16 flower morphology and nectar traits values along two main dimensions and measure the similarity between 26 native plants visited mostly by birds versus those by insects. We confirmed the pollination effectiveness of opportunistic birds. Quantitatively, birds were not important pollinators compared to insects. However, qualitative components of fitness improved when both birds and insects visited the flowers. We further reported two main flower types: entomophilous species, which are as expected to be mostly visited by insects, and a second group mostly visited by opportunistic birds that display mixed floral traits not fitting the classical ornithophilous syndrome. Flower shape, corolla size and nectar volume seem to be important for bird visitation in the plant community of the Galápagos. Our study underscores the importance of co-adaptation and floral diversification in non-specialized plant-visitor interactions.

Keywords: floral diversification, frugivory and seed dispersal, Microlophus spp., native Galápagos birds, pollination effectiveness

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[*] Speaker

Plant conservation on oceanic islands: scientific needs and examples of good practice to solve imminent challenges (Symp.)

Contents

Identifying a network of Tropical Important Plant Areas (TIPAs) in the British Virgin Islands

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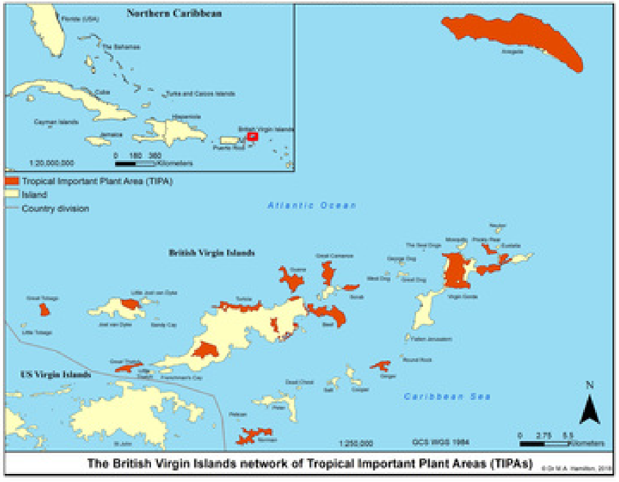
Map showing the network of 18 TIPAs across 13 islands of the British Virgin Islands archipelago.



The British Virgin Islands (BVI), a UK Overseas Territory in the Caribbean Sea, have more than 50 islands, keys and rocks. The territory is part of the Puerto Rican Bank Floristic Province that has an endemism of 13.6% with 292 endemic taxa, four of which are endemic to the BVI. The National Parks Trust of the Virgin Islands and the Royal Botanic Gardens, Kew, along with local and international partners, have been researching and working to conserve the plants of the BVI for over 20 years. The botanical expertise, species and habitat management skills and robust datasets on the local flora and terrestrial habitats generated during this collaboration created the opportunity for the group to embark on a three-year project to identify the BVI's Tropical Important Plant Areas (TIPAs). Baseline plant data and gap analysis identified priority species and islands that required further surveys. After completion of fieldwork and data collation, a total of 3688 geo-referenced high-resolution (+/-10m) records from herbarium specimens and field observations of the priority plant species were used to: (a) prepare and submit to the IUCN Red List of Threatened Species a total of 36 plant species assessments, including 25 globally threatened species; (b) identify highly restricted and range restricted endemics; (c) consolidate and agree a national list of 35 species of national high conservation importance. Analyses of land cover data identified five nationally threatened habitats in the BVI, each covering $< 10\%$ of the total national land area and in decline. Species and habitat data imported into a GIS were used by the BVI TIPAs national team during a series of workshops to apply the TIPAs criteria and identify a network of 18 TIPAs across 13 islands of the BVI archipelago. This recognition of BVI's important sites for botanical richness and threatened plant species and habitats, applying international standards to robust data, is an important tool for long-term species and habitat management to ensure the future of the BVI's unique flora.

Keywords: threatened species, plant diversity, threatened habitats, Caribbean, conservation

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The transition to selfing and its implications for the conservation of small insular plant populations: a case study from *Tolpis succulenta* in the Azores

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Baker's law posits that self-compatible (SC) plant colonizers of oceanic islands should be more frequent than self-incompatible (SI) colonists because sexually-reproducing populations can originate from a single SC colonizer whereas two or more SI compatible mates are necessary. SC is over represented in insular Asteraceae compared to mainland members; nevertheless, many speciose Asteraceae lineages originated from SI or pseudo-self-compatible (PSC, can set some self-seed) colonists. Members of the composite genus *Tolpis* endemic/native to the Macaronesian archipelagos, save one Canarian species, consist of SI/PSC species and are exceptions to Baker's law. Interestingly, the *in situ* transition to selfing in the dynamic landscapes of oceanic archipelagos has rarely been reported for native/endemic insular composites. The purpose of this study was to examine the breeding system of two small populations of *T. succulenta* on Graciosa Island in the Azores, where the species is exceedingly rare. Progeny of maternal plants from the two populations exhibit high self-seed set. Segregation for SI/SC in synthetic F2 hybrids between SC Graciosa plants and SI *T. succulenta* from the Azores showed one major factor associated with breeding system, with SC recessive to SI. Phylogenetic analyses of genomic markers resolved SC *T. succulenta* as sister to SI *T. succulenta* in the Azores, suggesting that SC originated from SI *T. succulenta*. Plants on Graciosa are morphologically distinct from SI *T. succulenta* on other Azorean islands, with smaller capitula and style branches, and lower pollen-ovule ratios. The likely major factor favoring selfing in these small populations is the paucity of compatible mates both during and subsequent to establishment on Graciosa. Lack of pollinators was ostensibly not a large factor because plants can set seed in the absence of floral visitors. The ability to set self-seed without pollinators has positive conservation implications for *T. succulenta* on Graciosa; the greatest threats to the populations are loss of habitat and invasive plants. Evidence for formal taxonomic recognition of populations on Graciosa include phenetic divergence, occurrence as distinct clades in the phylogeny, and the likelihood that they are genetically isolated by the SC breeding system and spatial/geographic divergence.

Keywords: Breeding system, conservation, Tolpis, Azores

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†Speaker

Conserving the threatened Puerto Rican endemic plant, *Varronia bellonis* (Cordiaceae)

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Varronia bellonis (Cordiaceae) in fruit on the Caribbean island of Puerto Rico

Omar Monsegur

Varronia bellonis (Cordiaceae) is a threatened plant species with a very restricted distribution on the island of Puerto Rico. Prior to our work, little was known about the status of natural populations, the species phenology, pollinators, seed dispersal or its habitat requirements with no investigations into its genetics or pollination syndrome. An international group is working to resolve the species taxonomic placement and develop phylogeographic and population genetic studies to develop management strategies for the species recovery. Before this study, around 40 collections lodged in herbaria since the species discovery in 1884 had wanting information about collecting locality and phenology. The IUCN Red List assessment for the species in 2014 as Critically Endangered estimated that there were only 47 mature individuals remaining in the wild based on available literature. Desk-based studies pulled together available resources into a GIS, including all available occurrence records, land cover maps from cloud-free Landsat imagery and surface geology data from the US Geological Survey. Field-based activities have been undertaken in and around the three historic locations known to have supported populations, including presence/absence survey, sampling for genetic analyses, camera trapping for plant-animal interactions and collection of habitat, phenological and morphological data. We found extant populations in and around the Maricao, Rio Abajo and Susúa State Forests and have documented several new individuals and previously unknown locations in Arecibo, San German and Utuado. The current estimate is circa 300 mature individuals. A strong correlation between the species recorded locations and specific geology and land cover types was observed suggesting the importance of habitat preference. We have secured *ex-situ* collections with seed stored in the seed bank at the University of Puerto Rico, Mayagüez campus. Camera trapping has revealed many animals interacting with the plant suggesting the importance of forest remnants for the species conservation. Our work is providing baseline information for developing a sound species recovery plan based on population genetics and the conservation status of remnants of preferred habitat. The project provides a framework for the collaboration on the conservation of regional endemics and for prioritizing the research needs of these species.

Keywords: Biogeography, Caribbean, conservation, Cordiaceae, recovery

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[*] Speaker

The conservation of New Caledonian rare and endangered species threatened by mining activities, the need of a global approach for a big challenge

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New Caledonia is a tropical archipelago located in southwest Pacific, and recognized as a hotspot of biodiversity. Within its exceptional flora (3389 species), about 20% have been recognized as narrow endemic species (NES). Locally, narrow endemism has been poorly studied, but is supposed to be linked with ultramafic soil, topography specificity, and climate diversity of the archipelago. Nevertheless, these species, more than others, are threatened by human-induced events, such as mining activity, bushfires, and alien species. In order to prioritize conservation actions for so many NES, we initiated several research programs from 2007 in order to define priority conservation areas, to develop a method to easily evaluate their potential distribution and to identify their nursery requirements for *in situ* reinforcement and *ex situ* preservation. All NES were mapped across New Caledonia, and " Hotspots of Narrow Plant Endemism " (HNPE) were defined as the areas containing more than 7 NES per 2-by-2 km square cell. Secondly, we modelled the potential distribution of 25 of the rarest species from Mount Kaala (one of the HNPE) using occurrence data from two sampling campaigns, and 8 high-resolution environmental predictors in a Species Distribution Model (SDMs) framework. Finally, ecological studies were conducted (phenology, population status, mapping, collection, germination) to propose management plans for these species.Distributional data produced on NES permitted to establish a map of "HNPE" and to identify locations in most urgent need for further conservation assessment and subsequent action. The method applied for modelisation on Mount Kaala permitted to support the ability of presence-only SDMs to predict areas of high conservation value using fine-resolution environmental layers and field-collected occurrence. After 2 years of activities on this area, there were nearly 800 surveys from field prospections, 10 species studied for their germination requirements with nearly 8 that led to the production of more than 200 plants. All these data allow to provide recommendations and to propose practical tools for the protection of rare and endangered species. It also permitted to enrich extinction risk assessment by the New Caledonia Plants Red List Authority.

Keywords: narrow endemic species, species distribution models, conservation action plans

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Ex situ seed conservation of Hawaiian 'exceptional species' as a case study for tropical island floras

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The Hawaiʻi Seed Bank Partnership conducts research on *ex situ* storage protocols for Hawaiʻi's native flora, and has gathered real-time data from hundreds of species for more than two decades. Seed storage behavior has been investigated, and 197 species have been assessed for seed freeze-sensitivity, a loss of viability in frozen storage (-18○C) when compared to refrigerated storage (5○C). A new index of Relative Performance was calculated with paired storage experiments at -18 and 5○C. Four Hawaiian families and 10 genera showed freeze-sensitivity or likely freeze-sensitivity. Additionally, we assessed 295 species for *ex situ* storage longevity. We recommend re-collection intervals, before viability falls below 70% of maximum germination, which range from > 20 to < 5 years, depending on the species. The largest family in the Hawaiian flora, Campanulaceae, is a spectacular example of adaptive radiation, with 159 endemic species in 6 genera from a single colonization, and over half are assessed as threatened on the IUCN Red List. The Hawaiian Campanulaceae is highlighted as a characteristic example of *ex situ* seed freeze-sensitivity and variation in longevity. This is the most comprehensive, long-term study to date on seed storage behavior and *ex situ* longevity for a regional flora. A high incidence of seed freeze-sensitivity is not yet known in any other region, so we present a protocol for testing seed freeze-sensitivity that can be utilized or adapted globally. Seed banking is now a critical tool for Hawaiian plant conservation, including these 'exceptional species' with freeze-sensitive seeds. Therefore, the Hawaiian flora can serve as a model for other tropical, subtropical, and island regions that might utilize seed banking to preserve species of conservation importance, now or in the future.

Keywords: Campanulaceae, freeze sensitivity, genebank, Hawaii, seed banking

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The IUCN Plant specialist group for Macaronesia: Using transnational cooperation and updated scientific data to better understand and mitigate the threats to oceanic island floras.

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Following the recent publication of thorough multidisciplinary reviews of current and emerging threats of the native floras of the Macaronesian region (encompassing the archipelagos of the Açores, Madeira and Selvagens, Canaries, and Cape Verde), a new Macaronesian Islands Plant Specialist Group (MISPG) was constituted for the period 2017-2020 under the IUCN Species Survival Comission to assess the most urgent priorities for the conservation of the native Macaronesian floras, and to improve the impact of conservation science and practice for a better preservation of plant biodiversity in this multi-national insular region. The talk will delve into the most important priorities identified by the participating specialists, emphasizing examples on the needs to enrich and update the IUCN red list information available, to provide expert advice to eradicate the most important threats to the floras (introduced mammals, invasive alien plants and other consequences of global changes), and to upscale and enforce the application of multi-disciplinary research results in the planning of in situ conservation actions, alongside with strategically designed outreach activities with relevant stakeholders and social actors whose cooperation is needed for the effective improvement and enforcement of the existing nature protection laws. Overall, this IUCN chair aims to put into practice the most urgent actions suggested by the most updated scientific evidence, entailing a collaborative framework that should encompass Universities, Botanic Gardens and Regional Administrations competent in the protection of the environment in the Macaronesian area.

Keywords: Conservation, IUCN, Macaronesia, oceanic islands

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The IUCN Seed Conservation Specialist Group: Connecting experts, identifying gaps, and developing best practices

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The IUCN Species Survival Commission (SSC) is a global network of more than 7500 scientific experts, working together to achieve ”A just world that values and conserves nature through positive action to reduce the loss of diversity of life on earth.” The SSC includes over 140 Specialist Groups, organized taxonomically, regionally, or by discipline. The SSC Seed Conservation Specialist Group (SCSG) was proposed at the 2016 IUCN World Conservation Congress and established in 2017, and its mission is to promote seed conservation by providing a network for knowledge-sharing in different ecosystems around the world, and aiding in prioritization, capacity building, and development of best practices. ”Seed conservation” is defined as banking and/or preserving seeds of wild species, particularly those that are threatened or near threatened, primarily for *ex situ* germplasm storage and future reintroduction. The SCSG is comprised of experts including native seed bank managers, conservation program managers, national/international coordinators, and other specialists from around the world, and Botanic Gardens Conservation International serves as its secretariat. The work we do reduces risks faced by species and ecosystems, and it improves the status of biodiversity by safeguarding ecosystems, species, and genetic diversity. Our primary targets for the 2016-2020 quadrennium are: (i) Actively recruit new members (https://www.bgci.org/plant-conservation/scsg), (ii) Create an online global Seed Conservation Directory of Expertise (2018) (http://www.bgci.org/plant-conservation/seedexpertise), (iii) Conduct and publish a regional and topical gap analysis of seed conservation expertise (2019), (iv) Create IUCN Guidelines on Seed Conservation (2020). Recruitment is ongoing, and membership is open to all who are interested in seed conservation.

Keywords: ex situ, expert group, genetic resources, seed conservation

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Red Lists and open data: how the New Caledonia Plant Red List Authority has brought together environment professionals, scientists and amateur experts

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New Caledonia is a French overseas archipelago administrated by three provinces, each responsible for the management of its environment. This fragmented jurisdiction has led to a management of the vegetation inconsistent with the geographic distribution of the native plant species, which is obviously rarely limited to a single province. In 2014, an informal group of botanists bringing together environmental managers, scientists, as well as passionate amateurs, proposed to assess the extinction risk of all native plant species by using the Red list methodology. Approved by IUCN and free from provincial boundaries, the Red List Authority of the New Caledonian Flora (RLA-NC) deeply altered the endangered status of the New Caledonian vegetation. In the past, expert appreciation was the only available tool to determine which species should be protected by provincial stakeholders. Nowadays, the local protection status can be based on the Red List status and the assessment carried out by the RLA-NC. To this day, an eye-opening 42% of the ca. 1500 assessed species are considered as threatened and undergo heavy anthropogenic threats such as bushfires, mining activities and invasive species. The RLA-NC is a very useful tool for federating stakeholders, gathering raw data and providing a more accurate picture of the taxonomy and distribution of plant species. Nevertheless, the in situ conservation of threatened species remains a challenge for managers who do not have the wherewithal to efficiently undertake species-by-species protection. We acknowledge that protected area planning is a more applied strategy in which the Red List of Threatened Species is an indispensable element. Finally, the least predictable success of RLA-NC was to become in just a few years a key authority that is consulted before any environmental decisions and whatever the legislative fragmentation.

Keywords: IUCN, New Caledonia, plant conservation, Red List

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Strategies for conservation of endemic species in protected areas of Cabo Verde islands

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Cabo Verde has a rich marine and terrestrial biodiversity, but most of the endemic groups have restricted geographic distribution and high vulnerability to threats, mainly due to the loss or alteration of their habitats. Establishment of conservation priorities in light of this environmental degradation requires sound knowledge on the distribution of biodiversity and identification of sites that are potentially important for conservation actions. Over the past decade, there have been some important successes including, the publication of the IUCN assessments for endemic plants and reptiles, and the establishment of the protected areas systems. In fact, the creation of the National Network of Protected Areas in 2003, allowed the elaboration of management tools to safeguard the unique biodiversity of Cabo Verde. Despite recent successful interventions, the management of the national protected areas system faces a number of problems, namely insufficient financial and staffing commitments. The purpose of this communication is to show several practical examples of how the implementation of the Network of Protected Areas in Cabo Verde has been promoting participatory approaches to biodiversity conservation. Particular emphasis is given to some Natural Parks where a great diversity of endemic species occur, namely in the: i) Fogo Natural Park, which occupies an area of 8,469 hectares in Fogo Island; ii) Natural Park of Serra da Malagueta with an area of 774 ha (Santiago Island); and the two Natural Parks of the Santo Antão Island (i.e. Natural Park of Cova / Paul / Ribeira da Torre, area: 2091.50 ha and Natural Park of Moroços, area of 818.10 ha). Finally we will discuss how present management activities done within these protected areas have contributed to the reintroduction of threatened endemic species in their natural habitats and to control the invasive exotic species.

Keywords: in situ conservation, IUCN Red List, Macaronesia islands, threatened species, vascular flora

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Conservation of crop wild relatives of Macaronesian Islands: current status and outlook

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In view of the expected future climate changes, it is of the utmost importance to broaden the gene pool of global crop species to increase their resilience to these possible changes. The contribution of Crop Wild Relatives (CWR) to improve crop performance is growing and has largely been achieved through the donation of useful genes for biotic and abiotic stress tolerance. However, CWR are becoming increasingly threatened in the wild and are inadequately conserved, both in situ and ex situ. The Macaronesian Islands (i.e. Azores, Canaries, Madeira and Cabo Verde) are among the top biodiversity hotspots in Europe, containing a relevant genetic diversity also as regards CWR. An effective conservation and utilization of this huge native biodiversity is dependent on the availability of, and access to, high quality ecogeographic information about each taxa (i.e., their distribution, biology, ecology and conservation status, with respect to the environments in which they grow), as well as their ex situ conservation status. In this communication, we present a checklist of the most important CWR of Macaronesian Islands and make comparative analyzes of their patterns of diversity across all the archipelagos. Specifically, we will provide new data to: i) characterize the CWR diversity in each archipelago, based on taxonomic, distribution and ecological data; ii) identify the most important CWR radiations within the Macaronesian Islands; and iii) determine potential areas of occurrence for these species. New data will be available to support the design of conservation tools/plans for prioritized CWR within the Macaronesian Islands.

Keywords: Agrobiodiversity, Biodiversity hotspot, Gene Pool, in situ Conservation, Prioritizing CWR taxa

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[*] Speaker

Seabirds on Islands (Symp.)

Contents

Seabird on islands: general overview and a case study

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We first make a review of what is known on the impacts of seabirds on islands (on soil, vegetation, invertebrates,...) and on adjacent marine habitats. We will then show how biological invasions (especially by introduced mammals like rats or cats), by reducing the number of breeding seabirds, can have cascading effects on an entire ecosystem. We present some clear evidence that island restoration projects consisting of eradicating introduced mammals not only benefit to seabirds but also to other seabird-driven interactions and components. In a second part we present the ecological changes (including native biodiversity recovery) observed on Tromelin Island 13 years after rat eradication. The study concerns seabird and vegetation monitoring as well as the study of the ecology and impact of mice (another introduced mammal, that we failed to eradicate). Overall, the seabird community changed drastically in terms of number of breeding species (from 2 species at the time of rat eradication in 2005 to 6 species in 2018) and in terms of bird numbers (from less than 300 breeding pairs to more than 3000 breeding pairs). Meanwhile, the vegetation changed in term of plant abundance, coverage and diversity. Other major factors like soil structure, climate and marine influences very clearly shaped the organization of the vegetation. Mice were very abundant and fed mostly on plants and insects. Recent observations suggest however that some mice may have changed their foraging behavior by attacking chicks of masked boobies. Based on these findings we built a conceptual model showing the interactions and retroactions between the various components of this naturally simplified island ecosystem (marine habitats, soil, climate, vegetation, introduced mammals and seabirds) and made some recommendations in terms of island restoration and management.

Keywords: island ecosystem dynamics, biological invasions, ecological restoration, plant – animal interactions

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[*] Speaker

Consequences of multi-species introductions on island ecosystems

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Multiple interacting introduced species are now the norm on islands across the planet, but the consequences of this for native species and ecological communities can only be properly understood if the mode of ecosystem regulation is taken in to account. In contrast to continents where predation-controlled top-down trophic regulation is the norm, islands are predominantly resource-limited bottom-up trophic regulated ecosystems, reliant on temporally-varying, externally-driven nutrient inputs. The outcome of interactions among introduced species on their population dynamics will depend on their relative trophic position, ultimately determining whether their combined impacts on native species are additive, multiplicative or suppressive of one another. Changes at different scales in community structure that occur following multiple introductions, and their effect on function, can be investigated from analysis of ecological networks. Understanding how both species population dynamics and community structure change following multiple species introductions to bottom-up regulated ecosystems will better inform appropriate conservation management strategies on islands. This will be particularly important when predicting the consequences of invasive species eradications, where an ordered ecological disassembly that minimises adverse effects in the wider community is to be preferred. Restoration targets can then be set that focus on removing or minimising the impact of keystone introduced species and re-establishing bottom-up trophic regulation dominance on islands. Although a robust understanding of the consequences of multiple species introductions to ecosystems requires extensive data, islands provide an opportunity where resolvable networks and consistent patterns in species introductions and interactions can facilitate predictability.

Keywords: conservation, eradication, interaction, invasive, restoration, trophic

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*Speaker

Seabirds on islands: unraveling drivers of spatial distribution for breeding seabird populations on New-Caledonia islets

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New Caledonia is a "French" archipelago in the Western Pacific comprising dozens of islands and $>$ 600 islets and is home to at least 23 breeding seabird species. The New Caledonian EEZ also contains the fourth largest Marine Protected Area, the Natural Park of the Coral Sea (1,292,967 km^2), which encompass several remote islet groups such as d'Entrecasteaux reefs and the Chesterfield archipelago. Despite long-term efforts in ornithological monitoring and several eradication campaigns targeting invasive mammals, drivers of breeding seabird communities and population abundance are yet poorly known. We aggregated data from 105 ornithological surveys (1958-2019) on 92 islets spread across New Caledonian waters to produce a local assessment of the community distribution of nesting seabirds. We then tested the effects of anthropogenic (invasive species, harbor distance, visitation) and non-anthropogenic (habitat characteristics) drivers on site-wise abundance and species richness. Finally, we used our results to evaluate the impact of past eradication campaigns on seabird distribution, discuss the relevance of extant conservation measures and identify sites that should be prioritized for future research and management. Overall, we found species richness and bird abundance to be strongly correlated with the distance to nearest harbor, with the most remote islets concentrating the largest and most diverse colonies. We also observed significant interspecific variation of breeding ranges (distance from harbor at which breeding occurs), that may account for differences regarding the tolerance to human presence and visitation. Our analyses were partly limited by data heterogeneity due to uneven islet coverage and the variety of survey methods used, and thus did not include temporal trends. To the best of our knowledge, this is the first attempt to identify drivers of breeding seabird distribution on islets covering most of the New Caledonian waters. Our findings highlight the importance of near-pristine sites for seabird breeding and emphasize the need for more comprehensive, fine-tuned conservation policies for maintaining breeding populations. Future developments include the addition of more study sites (Loyalty islands, Remote Eastern islands) and large-scale comparisons with other important seabird breeding locations in the Indo-Pacific area.

Keywords: island ecology, New Caledonia, seabirds, spatial distribution, conservation

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Behavioural ecology and impact of feral and domestic cats at a coastal seabird colony of Reunion Island: implications for conservation

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Cats are opportunistic predators responsible of the collapse of many animal populations on islands. Seabirds are particularly vulnerable because of their lack of any anti-predator behaviour. The site of Grande Anse (South of Reunion Island) holds the main breeding colony of wedge-tailed shearwaters (*Ardenna pacifica*) of the island and a colony of white-tailed tropicbirds (*Phaethon lepturus*). It is a touristic area with takeaways and restaurants surrounded by habitations. The area is frequented by both domestic cats and feral cats. Our goal was to investigate the behaviour of domestic and feral cats and their respective impacts on seabirds. We used four complementary methods: fine-scale tracking of cat foraging movements with GPS collars, automated observation of seabird nests with camera traps, cat scat analysis and the wedge-tailed shearwater's breeding success. The results show that domestic cats have small home ranges and do not forage at seabird colonies. Feral cats on the other hand have wider home range and frequently forage at seabird colonies. Cat tracking also revealed that feral cats very frequently foraged at the takeaways and restaurants, taking advantage of food garbage. The same cats alternatively forage at food garbage and at seabird colonies. Camera trap surveys showed that feral cats were very abundant at seabird colonies and some were seen attacking shearwaters. The breeding success of wedge-tailed shearwaters was low (39%). Scats analysis revealed that cats fed mainly on food garbage, rats, insects and occasionally seabirds. These results were confirmed by the finding of several dead shearwaters at the colony, most of them probably killed by cats. Our results show that domestic cats do not have a direct impact on seabirds. Feral cats on the other hand threatened coastal seabirds. Furthermore, takeways and restaurants represent an abundant and predictable source of food for feral cats and contribute to the high density of cats at seabird colonies. We propose adapted management guidelines for seabird conservation in this context: a better management of waste at restaurants and takeaways, a permanent control of feral cats and a sterilization campaign of domestic cats to avoid these cats to reinforce feral cat population by breeding.

Keywords: seabirds, tracking GPS, cats, biological invasion, management plan

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Seabird recovery following rat and cat eradication in Seychelles: achievements and challenges.

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The impact of rat and cat eradication on ecosystems is poorly documented, especially in the tropics. In Seychelles, between 1996 and 2010, invasive rats and (in most cases) cats were eradicated from ten islands (five granitic and five coralline), of 21 to 219 ha. Monitoring comprised formal protocols combined with empirical wildlife observations. To date, benefits have been documented for a minimum of 23 seabird populations of nine different species, i.e. 12 (re)colonisations and 11 population increases. Increases in population size or range have been recorded in almost all islands where rats (and cats) were removed. First positive impacts were noted within one to ten years after the eradications, in some islands more substantially than others depending on the proximity of source populations and other unknown factors. Almost all seabird populations already present increased in numbers, and six species established or re-established a total of ten new breeding populations across seven islands. Seabirds appear to play an important role in the ecosystem recovery process, by inducing vegetation changes and bringing in nutrients. Vegetation changes that followed rat eradication such as the rapid development of native *Pisonia grandis* trees further contributed to the establishment of new species or the increase of existing ones. Apart from seabirds, many other native vertebrates (landbirds, reptiles) and several large invertebrates (snails, millipedes, crabs) have also benefited from these operations, further contributing to the restoration process of these islands. Documenting ecosystem recovery should be given higher priority in future. Overall, rat and cat eradication consistently benefited seabird populations and island ecosystems in all cases. However, biosecurity is the keystone for long-lasting conservation impacts of such island restoration programs and crucially needs to become part of islanders' culture. Lack of surveillance and poor biosecurity can have dramatic consequences. The recent reinvasion of Conception Island by rats, the subsequent loss of one third of the global population of a threatened endemic passerine (Seychelles White-eye *Zosterops modestus*) and the decline of the recently established shearwater colony reveals how ecosystem recovery can be quickly reversed, and how vulnerable seabirds and other wildlife, which depend on predator-free island sanctuaries, are.

Keywords: cat eradication, ecosystem recovery, island restoration, rat eradication, seabird recovery

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Initial seabird response to an on-going rat eradication project on Lehua islet, Hawaii (USA)

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Lehua Islet is a Bird Sanctuary situated 19 miles off the coast of Kauai. Considered the most important seabird islet in the main Hawaiian Islands, Lehua has nine confirmed breeding seabird species including the only U.S. breeding population of Black-footed Albatross *Phoebastria nigripes* outside of the north-western Hawaiian Islands and a breeding population of the endangered Band-rumped Storm-petrel *Oceanodroma castro*. However, seabirds on the islet have been heavily impacted by the introduced Polynesian Rat *Rattus exulans*, which have also prevented native plant restoration efforts. In 2017 an ambitious multi-partner project was initiated to eradicate rats off Lehua, using aerial drops of the anti-coagulant rodenticide Diphacinone. To assess the impact of this island restoration effort, we present data on rat prevalence and seabird response by the end of 2018 using multiple techniques including burrow cameras, seabird plots, burrow monitoring and acoustic recording devices. Remote cameras indicate that a small number of rats are still present indicating that total eradication may not have been achieved. Despite this, the rat population has been dramatically suppressed and seabird response to this is considered in terms of estimated population sizes, reproductive success rates and breeding distribution for multiple species. In particular, the smaller seabird species appear to have benefited the most from the eradication effort, with the number of breeding Bulwer's Petrel *Bulweria bulwerii* burrows and their respective reproductive success being significantly higher in 2018 than previously. With these results in mind, we discuss possible directions for the Lehua Islet Restoration Project in 2019 and beyond.

Keywords: rats, eradication, Hawaii, seabird, restoration

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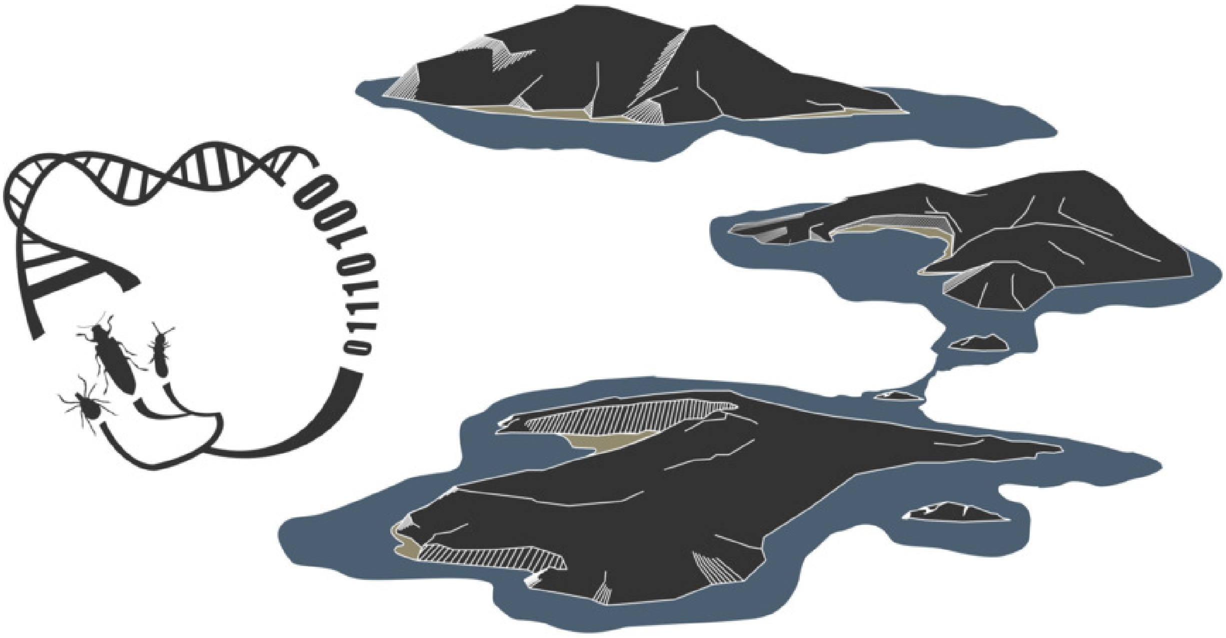
Synthesizing island biodiversity theory for community-wide genetic data (Symp.)

Contents



Origins of diversity on islands: the nexus of ecology and evolution in community assembly

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Research on the dynamics of biodiversity has progressed tremendously over recent years, though in two separate directions – ecological, to determine change over space at a given time, and evolutionary, to understand change through time. Integration of these approaches has remained elusive, due both to the difficulty of dealing with more than a few taxonomic groups at a time within a given community, as well as the inability to measure ecological attributes of communities over extended evolutionary time. However, we now have ways to address these issues using archipelagoes with a known geological chronology that provide an opportunity to study ecological interactions over evolutionary time. Within this framework, technologies of next-generation sequencing are allowing estimates of abundance and diversity of entire communities of organisms, while theoretical developments can provide constructs for interpretation of patterns of change through time. We use metabarcoding data from entire arthropod communities generated across sites of different geological age across the Hawaiian Island chronosequence. The data provide information on diversity, abundance, and habitat associations. We examine these patterns across the islands to assess the dynamics of community assembly over time. Results indicate that species abundance distributions deviate from expectations at different stages (or ages) of community development; likewise, network structure over the island chronosequence changes in a fairly predictable manner. Within the theoretical construct, the data allow us to understand the dynamics shaping community structure over extended time and provide insights into how communities might be expected to accommodate changes in the future as island communities are confronted with biotic homogenization. The results have key implications for assessment of the status of biological communities and approaches for conservation and restoration.

Keywords: arthropods, evolution, Hawaiian islands

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Island biogeography and the distribution of genetic variation in ecological communities

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Biodiversity in ecological communities can accumulate via colonization from a regional source pool, *in situ* speciation, or some combination of these. Reconciling the relative importance of these processes is hindered partially because the two extremes are currently the domain of different fields of study. *In situ* speciation is commonly studied through the lens of phylogenetics and trait evolution, whereas communities assembled via colonization are the focus of neutral and non-neutral models of community ecology. Population genetic variation at the community scale has been rarely studied, and could provide a complementary axis of information to aid in disentangling processes shaping ecological communities. To this end I introduce a mechanistic model of community assembly that roots itself in classic island biogeography theory (MacArthur and Wilson 1967; Hubbell 2001) to make historically dynamic joint predictions of observed data along three axes that unify macro-ecology, phylogeography, and macro-evolution: species richness and abundances; genetic diversities and divergences; and trait evolution within the context of phylogenetic diversification. Using simulations and empirical data I demonstrate that each data axis captures information at different timescales of assembly, and that combining all these axes results in much finer resolution inference. Finally, I demonstrate a simulation-based inferential framework (massive eco-evolutionary synthesis simulations; MESS), which combines ABC and supervised machine learning to test competing models of community assembly and evolution (niche vs neutral and evolved vs assembled) and to estimate an array of model parameters relevant to a complex history of island assembly and evolution.

Keywords: Community genetic diversity, Species abundance distributions, Island biogeography, Ecological neutral theory, Non, equilibrium dynamics

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*Speaker

Assessing the drivers of biodiversity patterns using environmental DNA data: macroecology and macroevolution of the oceanic plankton

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Recent oceanic surveys have collected genetic datasets that are at the same time community-wide, i.e. representing all species from a community assemblage, and global, i.e. covering a large part of the total diversity of clades. These data offer an unprecedented opportunity to assess the ecological and evolutionary drivers of biodiversity patterns, from local communities to the global ocean. I will present two studies based on data from the TARA Ocean Global Expedition. The first focuses on the drivers of diversification of the oceanic plankton; the second focuses on the drivers of community assembly. These studies will illustrate recent quantitative tools for studying diversification and community assembly. Next, I will discuss future avenues for integrating these quantitative tools for a more inclusive understanding of biodiversity patterns.

Keywords: diveristy, oceanic plankton, distribution, NGS, environmental DNA

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*Speaker

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Diversifying as a holobiont: macroevolutionary patterns of microbiota in an island archipelago

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Plants and animals from island archipelagos often display a specific phylogeographic pattern, called the *progression rule*: their current biogeography along the island chronosequence reflects their past evolutionary history of repeated migration events followed by allopatric speciation and radiation. While the progression rule has been well documented in macroorganisms, whether the microorganisms associated with these hosts – their microbiota – also follow the progression rule remains unclear. In addition to dispersal ability and mode of diversification, the biogeography of the microbiota on island archipelagos will depend on mode of transmission, i.e. whether the microbes are independently acquired from the environment during the life of their hosts (i.e. environmental acquisition), transmitted across populations or species by host-switch (i.e. horizontal transmission), or transmitted across generations associated with their hosts (i.e. vertical transmission). Here, we aim to document and explain phylogeographic patterns of the arthropod host associated microbiota on island archipelagos. First, we build upon a model that we recently developed for characterizing symbiont inheritance during host-microbiota evolution. In this model, microbial sequences evolve on a fixed host phylogeny; they are vertically transmitted and can experience horizontal host-switches. Adjusting this model to microbial sequence alignments mapped to host phylogenies allows studying microbial modes of inheritance. We further develop this model in order to account for the geographical distribution of host species on islands in the process of vertical transmission and host-switches. Second, we analyze gut microbiota data of *Ariamnes*spiders. These spiders experienced a recent adaptive radiation along the Hawaiian archipelago. We describe the microbiota's phylogeographic pattern, assess whether it follows the progression rule, and attempt to explain the phylogeographic pattern by analyzing modes of inheritance using our model. Finally, we discuss how modes of inheritance of the microbiota could impact host evolution in the context of island archipelagos.

Keywords: biogeography, microbiota, diversification, island archipelagos, mode of transmission

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[*] Speaker

Whole-community assembly from metabarcoding data reveals the structure of the soil mesofauna at multiple genetic levels and spatial scales

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Soils are among the most diverse habitats on Earth, but at the same time they are the most poorly studied terrestrial ecosystems. Our understanding is extremely limited for the arthropod mesofauna, because conventional morphological and molecular approaches are in many cases insufficient for the characterisation of their complex communities. The implementation of high-throughput sequencing for metabarcoding now offers unprecedented opportunity to overcome past constraints to characterise and understand soil biodiversity, but its application is still very limited and mostly constrained to the OTU (species) level. Here we take advantage of newly developed protocols for sample-processing and bioinformatics to generate community-wide genetic datasets for soil mesofauna, to explore whole-community assembly of belowground biodiversity, both at and below the species level. Our analyses across continental (western Europe) and island (Canary Islands) settings uncover a strong geographical structuring of soil communities at multiple genetic levels, and reveal a fractal pattern in soil community assembly. This aligns with a predominance of neutral but limited dispersal driving community assembly of soil mesofauna from landscape to broad geographical scales. Our results cast light on the open question of whether the distribution of above- and belowground biodiversity is governed by the same laws, and provide an empirical and analytical benchmark to identify the generalities and singularities of continental and island biodiversity dynamics.

Keywords: community assembly, metabarcoding, soil mesofauna, neutral processes

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[†] Speaker

Trait dependent diversification on islands (Symp.)

Contents

A global review of insular woodiness and its impact on diversification

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Woody species not only dominate most continental ecosystems, but also (sub)tropical islands are known to be proportionally more woody than the flora of adjacent continents. It is unclear, however, why some plants are woody and others herbaceous, probably because wood formation is a complex process that can be triggered in different and largely understudied ways.

As a first essential step to solve this evolutionary puzzle, we need to know what are the woody species that have evolved from herbaceous relatives on continents (derived woody species) and islands (insular woody species), and what are the hotspot regions of derived woodiness. Therefore, the presenting author has recently compiled a global derived woodiness database in angiosperms based on published phylogenies, taxonomic revisions and flora treatments. The database comprises nearly 7000 derived woody species of which 1789 are island endemics. Most of these island endemics are insular woody in the strict sense, meaning that the wood development has occurred after arrival of the original (herbaceous) colonisers. The families that have contributed most to insular woodiness across archipelagos are Asteraceae, Gesneriaceae and Plantaginaceae. Interestingly, many spectacular examples of island radiations consist of insular woody lineages, such as *Cyrtandra* (245 sp), *Veronica* (125 sp) and *Sonchus* (64 sp). However, another species rich island lineage, the Hawaiian lobeliads (131 sp), has evolved its woodiness outside the archipelago (and is therefore not insular woody in the strict sense), and there are several examples of monotypic insular woody genera with narrow endemics. Likewise, we see much variation across islands-archipelagos in terms of number of insular species: Canary Islands are ranked number one (258 sp), followed by Hawaii (210 sp) and New Zealand (165 sp), while New Caledonia surprisingly harbours only a handful of insular woody species.

In conclusion, insular woodiness can be linked with diversification for many of the spectacular island radiations, but it may well be that insular woodiness could lead to an evolutionary dead-end scenario for other island lineages. Future diversification analyses based on in-depth molecular phylogenies of island lineages will shed more light into the relationship between insular woodiness and diversification.

Keywords: angiosperms, insular woodiness, diversification

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The dark side of the island rule or how traits acquired on islands make endemic species more vulnerable to extinction

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Islands contribute disproportionally for their area (5% of the emerged lands) to world biodiversity (25% are insular species), but even more disproportionally to the worldwide-endangered species lists (60%) or to the worldwide post-description extinctions (75%). The insular contribution to pre-description extinction is not yet quantified, although it is expected to be similar. But actually, which are the reasons behind this fact? Besides the genetic threats, such as inbreeding depression or loss of heterozygosity, unavoidable related to any founder event, the common demographic structure of insular species, i.e. few, genetically structured populations, largely confined to a single island (SIE = single island endemics), usually with a small number of individuals, add increasing vulnerability to the island biota. Furthermore, many of the characteristics that island species acquire through evolution in isolation -the so-called island rule or insular syndrome- yield to increased species vulnerability towards both natural -volcanic activity, gravitational landslips, tsunamis and cultural or anthropogenic related events. Such island-syndrome traits that make island species especially vulnerable, affect both insular animal (gigantism, dwarfism, flightlessness, tameness, diminution of clutch size, relaxation of defensive behavior, etc.) and plant species (loss of dispersibility, insular woodiness, loss of defense against herbivory, trend to sexual dimorphism, etc.). Human related impact on insular species, either direct habitat destruction, degradation or fragmentation, overexploitation, hunting, fishing, pollution, collecting introduction of alien species, including disease vectors and diseases, climate change or trophic cascades, have shifted the continental megafauna extinction towards an insular megafauna and megaflora extinction, whose onset coincides with the human colonization of oceanic islands and micro-continents, what happened during the last 3 millennia and is still ongoing. The result is the demise of many insular charismatic species that have vanished forever.

Keywords: animals, extinction, island syndrome traits, oceanic islands, plants

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*Speaker

Detecting trait-dependent diversification

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Islands often host spectacular radiations. One explanation is that key innovations occur on islands that allow the exploration of new niche space. However, there are currently no methods available to test these ideas for islands with several independent colonizations. For global radiations such tests do exist. Here we present a new tool to analyze such global radiations and apply it to an island-like system, cichlids in Lake Tanganyika. The tool, called SecSSE (Several Examined and Concealed States-dependent Speciation and Extinction), requires phylogenetic data and trait data of the species at the tips; we have made it available as an R package. We ask whether depth-range generalists speciate at a different rate than depth-range specialists (shallow-water specialists or deep-water specialists), and whether depth range changes during speciation. We find that generalist species diversify much faster than specialists, but speciation does not involve change in depth range. Furthermore, shallow-water specialists seem to be a macro-evolutionary endpoint. We discuss the potential of this method to be used for multiple insular colonizations.

Keywords: phylogenies, diversification, SSE, model, macroevolution

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†Speaker

Frugivory-related traits promote island radiations of tropical palms

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Animal-mediated seed dispersal by frugivorous birds, bats and mammals is central to the ecology and functioning of ecosystems on islands, but whether and how frugivory-related traits have affected plant speciation on islands remains little explored. Small-fruited plants (i.e. fruits $<$ 4 cm) predominantly rely on seed dispersal by small-sized frugivores, such as birds, bats and small-bodied mammals. These small-sized frugivores show restricted dispersal with occasional long-distance dispersal, which may cause disrupted gene flow among plant populations and therefore increase the probability of genetic differentiation and allopatric speciation. Similarly, dispersal to isolated oceanic islands may facilitate speciation.

Using a global species-level phylogeny with comprehensive data on fruit sizes and plant species distributions in a comparative framework, we test whether fruit size and island distributions have affected speciation rates of palms (Arecaceae, ca. 2500 species), a plant family characteristic of tropical rainforests. Globally, the results reveal that palms with small fruit sizes have increased speciation rates compared with those with large (megafaunal) fruits. Interestingly, speciation rates of small-fruited palms are particularly high on oceanic islands in Southeast Asia, Australasia and the Pacific.

These results suggest that small fruit sizes may have facilitated the colonisation of isolated islands by strong-flying, ocean-crossing frugivores (e.g. frugivorous hornbills, fruit pigeons and fruit bats), with subsequent speciation of small-fruited palm lineages. Thus, frugivory-related traits in combination with geography and the movement behaviour of frugivores can influence evolutionary radiations of fleshy-fruited plants.

Keywords: diversification, fruit size, frugivory, plant, animal interaction, speciation

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The role of traits in non-adaptive diversification: some insights from a continental archipelago.

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The role of traits in diversification is primarily addressed within a macroevolutionary framework, where certain clade-specific traits are linked with increased diversification rates. Comparative phylogenetic tests can be very powerful for gaining an understanding of trait-dependent diversification patterns, but do not provide explicit links with the underlying microevolutionary processes. Comparative population genomic studies under an appropriate study design have the potential to bridge this gap, providing insights into the role of traits in driving divergence at the microevolutionary level. Here we use a comparative phylogeographic/population genomic approach to provide insights into the role of ecological traits in driving non-adaptive diversification of darkling beetles (Coleoptera: Tenebrionidae) across the Aegean archipelago. Previous results of the presenting author identified habitat preference as a key trait determining diversification of flightless darkling beetle lineages across the Aegean islands. Here we review the existing evidence, by re-analysing published and unpublished phylogenies of 15 darkling beetle genera. We delimit independently coalescing groups in each clade and estimate divergence times across the major geological barriers, which demonstrate that (a) stable-habitat specialist lineages are consistently deeply subdivided across the major geological barriers, (b) ephemeral-habitat specialists maintain species cohesion with shallow subdivision across the major geological barriers and (c) generalist lineages show intermediate levels of phylogeographic subdivision. We further examine more closely the microevolutionary processes at the early stages of diversification, by focusing on population divergence across an island group that has undergone cycles of fission-fusion during the Quaternary sea-level oscillations. We generate genome-wide SNP data (from ddRADseq) for five darkling beetle species sampled across nine present-day islands, which have been connected during low sea-level periods, and analyse them using coalescent-based demographic inference. The results show (a) deep divergence times and low levels of gene flow among populations of stable habitat specialists, (b) strong population bottlenecks in ephemeral-habitat specialists and (c) higher levels of gene flow among populations of habitat generalists. Our results highlight the importance of trait-mediated population persistence and gene flow in diversification and more generally the utility of combining micro- and macroevolutionary perspectives for a better understanding of the diversification process.

Keywords: Aegean, Coleoptera, comparative phylogeography, demographic inference, habitat preference

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Regular sessions

Atmosphere - biosphere - geosphere interactions

Contents

Will climate change shift tropical montane cloud forests upwards on islands?

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Island tropical montane cloud forests (TMCFs) host a disproportionally high share of the global biodiversity and provide critical ecosystem services to vulnerable insular societies. However, this ecosystem is imperiled by anthropogenic impacts including climate change that might push TMCFs towards higher elevations. The elevation at which TMCFs start varies greatly among islands and may depend on topographically driven local climate, which may in turn be influenced by large-scale climate. Thus, a necessary prerequisite to assessing the vulnerability of island TMCFs to climate change is to determine the role of island features versus regional climate in influencing local climate at the lower TMCF ecotone. An extensive literature review of the elevation at which island TMCFs start was undertaken. This elevation was modelled as a function of the altitude of the lifting condensation level (LCL) imposed by regional climate, island maximum elevation and upwind forest loss over the past 15 years. The elevation of the lower TMCF boundary was found to have been reported for 93 islands worldwide. TMCFs start from as low as 300 m on the small islands of Kosrae (Micronesia; maximum elevation = 628 m) and Aneityum (Vanuatu; 852 m) to a maximum of 1,600 m on the large islands of Cuba (1,974 m) and Hispaniola (3,175 m), providing a spectacular example of the 'Massenerhebung effect'. Both regional climate (LCL altitude) and island features (maximum elevation) influenced the elevation of the lower TMCF boundary, and these variables together accounted for 79% of the variance. On islands, climate change is likely to cause significant but small upslope shifts of the LCL and subsequently of TMCF lower boundary elevation in the future (+4.4 m for each 1○C increase in temperature). TMCF clearing and biological invasions might appear to be more pressing threats.

Keywords: global change, Lifting cloud layer, tropical montane cloud forest

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*Speaker

The challenges of measuring cloud liquid water content and cloud water interception in tropical montane cloud forests

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Tropical montane cloud forests (TMCFs) are important ecosystems that serve as havens for diverse biota and act as a water source for mountain watersheds. The contribution of wind-blown cloud droplets intercepted by TMCF vegetation to the hydrological input of these ecosystems and watersheds is difficult to measure, but important to know given the threats of climate warming, land cover change, and species invasion. Despite recognition of the importance of TMCF hydrology, field measurements of cloud water interception (CWI) and related variables are relatively sparse, in part, because of the difficulty in making reliable observations. The canopy water balance approach can be used to estimate CWI based on measurements of above-canopy precipitation, below-canopy net precipitation (throughfall plus stemflow), and estimates of wet canopy evaporation. To enable estimation of the spatial patterns of CWI, it is useful to measure not only CWI at representative sites, but also wind speed and cloud liquid water content (LWC). The product of those two variables yields cloud water flux (CWF) which, combined with parameters describing the vegetation, can be used to simulate spatially and temporally varying CWI. LWC sensors are generally quite expensive. Therefore, we tested the use of the relatively inexpensive Juvik-type passive fog gauge and an anemometer to estimate CWF and LWC. We found that fog-gauge-derived estimates were well correlated with highly accurate LWC measurements from a phase Doppler interferometer (PDI), although the inferred fog gauge catch efficiency was much lower than expected at approximately 13%. Based on these results, we estimated LWC and CWF based on fog gauge and wind speed measurements at five sites in Hawai'i. Results show varying means and diurnal patterns depending on location relative to topography, elevation, and wind direction. In follow-on analysis, these results will be used to estimate the spatial patterns of CWI across TMCFs of the Hawaiian Islands.

Keywords: cloud liquid water content, cloud water interception, fog drip, fog gauges, tropical montane cloud forests

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*Speaker

Cloud water interception and resilience of tropical montane bryophytes to climate change in cloud forests of La Réunion

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Tropical montane cloud forests (TMCFs) are characterized by frequent cloud immersion, host a high diversity of global biodiversity and provide vital ecosystem services to insular populations. Climate change on islands, is expected to both raise the cloud height base as a result of temperature increase and to increase the frequency of extreme events like drought. Bryophytes contribute a significant biomass in these systems yet the role of cloud water and the resilience of bryophytes to drought in island TMCFs is still poorly known. In La Réunion, we implemented a novel method to follow cloud water interception by bryophytes in the TMCF using *in situ*lysimeters. We showed that two abundant TMCF liverworts possess an excellent ability to intercept and store cloud water, and that stored water fluctuated according to climatic conditions. In order to better understand the ecophysiology of TMCF bryophytes, we examined chlorophyll fluorescence, under laboratory conditions, for 16 bryophyte species in response to dehydration and rehydration. This was accompanied by measurements of water retention capacity and relative water content of each species. Highest Water Retention Capacity and Relative Water Content were recorded for *Sphagnum*sp (2174 %: 91,37 %) and *Anthoceros*sp (1540 %; 7815 %). Dry down curves showed that species with high water storage capacity are favored by maintaining longer optimal photosynthetic activity. After one week of desiccation, half of the species could recover 50 % of their optimal photosynthetic activity within 24 h of rehydration. Most species, after 7 weeks of desiccation, could not recover their original photosynthetic activity after rehydration. These experiments highlight the presence of various strategies for managing desiccation by TMCF bryophytes at the microhabitat level. Bryophytes inhabiting the TMCF, exhibit a strong strategy in either tolerance or drought avoidance or a combination of both strategies, indicating a better adaptation to drought than expected. However, impact of repetitive drought on the physiology of the TMCF species remains unknown. The multiplicity of responses recorded for TMCF bryophytes regarding their physiology and life forms indicate that climate change will have distinct impacts on species.

Keywords: atmosphere/biosphere, chlorophyll fluorescence, ecohydrology, photosynthetic activity

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Preliminary results from the FARCE 2015 campaign: multidisciplinary study of the forests-gases-aerosols-clouds system in the tropical island of La Réunion

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The Forests gAses aeRosols Clouds Exploratory (FARCE) campaign was conducted in March-April 2015 on the tropical island of La Réunion. For the first time, several scientific teams from different disciplines collaborated to provide reference measurements and characterization of La Réunion vegetation, (biogenic) volatile organic compounds (BVOCs), (bio)aerosols and composition of clouds, with a strong focus on the Maïdo mountain slope area. The main observations obtained during this two-month intensive field campaign are summarized. They include characterizations of forest structure, concentrations of VOCs and precursors emitted by forests, aerosol loading and optical properties in the planetary boundary layer (PBL), formation of new particles by nucleation of gas-phase precursors, ice nucleating particles concentrations, and biological loading in both cloud-free and cloudy conditions. Simulations and measurements confirm that the Maïdo Observatory lies within the planetary boundary layer from late morning to late evening and that, when in the PBL, the main primary sources impacting the Maïdo Observatory are from marine origin via the Indian Ocean and from biogenic origin through the dense forest cover. They also show that i) the marine source prevails less and less while reaching the Observatory, ii) when in the PBL, depending on the localization of a horizontal windshear, the Maïdo Observatory can be affected by air masses coming directly from the ocean and passing over the Maïdo mount slope, or coming from inland, iii) bioaerosols can be observed in both cloud-free and cloudy conditions at the Maïdo Observatory, iv) BVOCs emissions by the forest covering the Maïdo mount slope can be transported upslope within clouds and are a potential way of secondary organic aerosols formation in aqueous phase at the Maïdo Observatory. These results largely contributed to the setting up of the OCTAVE 2017-2019 (Oxygenated Compounds in the Tropical Atmosphere: Variability and Exchanges) and Biomaïdo 2019-2021 projects. These projects will provide new material for the study of nucleation processes, sources and seasonal cycles of VOC and halogens from forests and the ocean, and will focus on the contribution of the aqueous reactivity to the secondary organic aerosols' (SOA) budget.

Keywords: biogenic emissions, clouds, secondary organic aerosols, Tropical forests

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*Speaker

Climate change in the southwest Indian ocean: observations and projections

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1

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Observations over La Réunion island during the past 50 years indicate a +0,17◦C temperature increase per decade. It is a worldwide issue already bringing catastrophic results in ecologically vulnerable regions. Climate projections at coarse resolution have previously been exploited over the basin using the Fifth Coupled Model Intercomparison Project (CMIP5) of the Intergovernmental Panel on Climate Change (IPCC). They indicate a consistent regional warming response during the 21st century. In the RCP4.5 scenario, warming should remain in a range between +1.0 and +2.0◦C (reference period 1971-2000). In the RCP8.5 (or pessimistic) scenario, temperatures could increase between +2.5◦C over ocean areas and +4◦C over land. Signals on future precipitation evolution are much less consistent with some contradictory signals especially during the rainy season. A large consensus nevertheless indicates a future decrease of precipitation during the winter season over the southern part of the South-West Indian Ocean (SWIO) region.

Small islands such as Mauritius, Seychelles, Comoros and La Reunion are not well represented by the coarse resolution (typically 200 km) of global climate models. To define adaptation strategies consistent with local issues (e.g., biodiversity conservation), it is therefore crucial to "downscale" (or refine) the information of global simulations at high resolution and evaluate the impacts of regional climate drivers (e.g., land/sea contrasts) at local scale over the different countries of the SWIO region. Through the framework of the "Adapt'action" facility, a new project named BRIO (Building Resilience in the Indian Ocean) has been funded by the Agence Française de Développement (AFD), in cooperation with Météo-France and the Indian Ocean Commission (IOC). This 2018-2020 project aims at supplying long-term regional climate simulations for the Southwest Indian ocean as well as training for regional experts on that matter. One of the project's final objective is to provide a set of 21st century high quality climate-related data on a free-access online regional portal. The idea is to develop user-oriented climate services for various sectors (including health, agriculture, energy and possibly ecology) at the regional and local scale, following community feedback.

This talk will present previous projections from CMIP5 over the SWIO as well as the BRIO project.

Keywords: Climate change, obervations and projections, temperature, precipitation, tropical cyclones, southwest Indian Ocean

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Satellite based oceanic monitoring around Reunion Island for the years 2003 to 2017

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Coastal waters are structurally and functionally diverse hotspots of marine biodiversity. In La Reunion Island those ecosystems are characterized by frequent disturbances. Severe cyclonic storms, increasing human activity and land-use change cause multiple effects including chemical and biological pollution as well as physical destruction along the coast line. In addition, ongoing climatic changes affects marine ecosystems. In order to characterize the spatial and temporal evolution of the coastal waters around La Reunion Island we investigated optical characteristics of several sea water quality parameters. Those include the diffuse attenuation coefficient at 490 nm (Kd490), particulate organic and inorganic carbon (POC, PIC), chlorophyll a concentration and night time as well as day sea surface temperature (NSST, SST). In this study, water quality indicators were derived from daily satellite imagery data from the Moderate Resolution Imaging Spectroradiometer (MODIS) in a spatial resolution of $\approx$ 2 km for the years 2003 to 2017. SST around La Reunion increased reaching +1$\circ$C in the south of the research area in 14 years. Water turbidity (Kd490), POC and chlorophyll *a* show high intercorrelations and indicate the presence of living material (phyto- and zooplankton, bacteria). They exhibit decreasing trends over the course of our investigation. The absolute concentrations as well as the coefficients of variation are elevated along the island's rainy eastern coastline which indicates the presence of a dynamic oceanic ecosystem. CaCO3 (PIC) concentrations are highest in the shallow waters of the western lagoons where it's concentration decreased by an average of 0,00009 mol m-3 in the marine reserve. Potential underlying reasons are coral bleaching or macrophytic algae decrease. The ocean productivity is highest in an area of 18 km in diameter around the island. For the years 2003 to 2017, it decreased at the eastern coast while the temperature rose. This phenomenon may influence fishing rates as well as the behavior and migrations of marine megafauna. Future conditions might promote biological invasions. The coastal ecosystems are changing with the climate. It is important to assess and improve the monitoring of the following stages of this phenomenon to help preserve human life quality and native biodiversity.

Keywords: climate change, coastal ecosystems, ocean remote sensing

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Biogeography

Contents

Functional disharmony of the flora of New Caledonia: filtering effect of ultramafic soils and metal accumulation syndrome

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New Caledonia, an archipelago in the Southwest Pacific, is renowned as one of the world's most significant biodiversity hotspot. The archipelago is also recognized as a hotpot for plants growing on metal-rich soils, as more than 70% of the endemic flora and 63% of species occur on ultramafic (*i.e.* metal-rich and nutrient deficient) soils. The chemical and physical adversity of ultramafic soils have driven some plants into spectacular transformations, including the evolution of trace element hyperaccumulation. The syndrome is known from many species in New Caledonia, although a systematic assessment is currently lacking. To gain insight into the full diversity of hyperaccumulation we determined metal concentrations (nickel and manganese) of the entire ultramafic flora using X-ray Fluorescence Spectroscopy (XRF) in herbarium specimens (NOU). This assessment comprises of a total of ≈11 200 specimens in 35 orders, 96 families, 281 genera, 1484 species covering 88.5% of the ultramafic flora. The mass screening resulted in the recording of 92 Ni and 70 Mn hyperaccumulator taxa, belonging to 12 and 22 families respectively; confirming that New Caledonia is a hotspot for these globally rare plants. Hyperaccumulator plants are phylogenetically clustered in a few major clades, especially the Oxalidales and Malpighiales, followed by the Proteales, Gentianales and Ericales. At lower taxonomic ranks, there is a strongly unbalanced distribution of hyperaccumulators in few major families (*e.g.* Phyllanthaceae, Cunoniaceae), and even few genera (*e.g. Phyllanthus*). The disharmony of the New Caledonian flora has been ascribed to the over-representation of groups associated with ultramafic soils, which might have been accentuated by the evolution of metal accumulation syndrome in a few distinct lineages. The results of this study suggest that ecological filtering and physiological prerequisites to metal-enriched soils have been of major importance in the phylogenetic assemblage of the flora. Several distinctive biogeographical factors of New Caledonia (*i.e.* the extend and old age of ultramafic soils, the isolation of ultramafic massifs) might have further promoted diversification and

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endemism of (pre-)adapted lineages. Current lines of research aim to explore the adaptive benefit of hyperaccumulation, in particular elemental allelopathy and plant-insect interactions in selected model groups.

Keywords: disharmony, ecological filtering, hyperaccumulation, phylogenetic clustering, ultramafic substrate.

A functional biogeography approach to insular bird communities with mixed-origin species

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Species introductions on islands result into heterogeneous assemblages with short common biogeographic histories, yet potentially redundant ecological functions. How native and feral species interact over resource and habitat in the absence of long co-evolutionary histories presides to the deterministic part of assembly processes in these assemblages, in turn affecting strategies to preserve indigenous biodiversity. Critical to this question are the ability of introduced species to cope with novel environments and their degree of niche separation with native species, which may or not permit local invasion. These processes can be investigated by studying shifts in alien species' ecological trait space between their native and introduction ranges, and its degree of overlap with co-occuring native species on introduction grounds, accounting for the depth of their common phylogenetic histories. Previous results suggested that insular assemblages are driven either by past competitive exclusion, habitat filtering or niche displacement associated with post-introduction lability in species' trait space. We attempt to disentangle these processes in New Zealand bird assemblages, which uniquely mix species from multiple biogeographical origin and range from narrow endemism to colonizing alien birds. New Zealand thus hosts some of the world's most peculiar bird assemblages, albeit without obvious conflicts among species with differing local histories. We use a multispecies hierarchical bayesian model fitted on 501 point counts to investigate niche separation between 21 alien and native species through their responses in abundance to habitat composition at landscape (proportion of native and man-modified habitats) and local scales (forest composition and vertical structure). Complementarily, we investigate the roles of species' ecological trait space and biogeographical origins in these responses through an ordination framework constructed with literature data. Our results support habitat filtering operating simultaneously at multiple scales, associated with trait-based separation between native and alien species. We further present preliminary results on the contributions of biogeographic origin and phylogenetic relatedness to habitat-trait associations in New-Zealand bird assemblages, and eventually propose avenues to refine these results through novel curve analysis methods. Our framework aims to integrates functional and biogeographic perspectives on novel insular communities to the benefit of a better understanding and conservation of island biodiversity.

Keywords: alien species, birds, ecological trait space, functional biogeography, New Zealand

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Dispersal modality determines the relative partitioning of beta diversity in spiders on a subtropical land-bridge archipelago

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Species diversity on islands is the result of colonization, extinction and speciation. Beyond the classical approach of alpha diversity, beta diversity partitioning provided fresh insights into the assembly mechanisms that drive the extent of change in community composition on islands. To identify geographical drivers determining the relative partitioning of species replacement and richness difference or nestedness-resultant components of beta diversity in spider groups with differing dispersal modalities (frequent, occasional or non-ballooners). We sampled spider assemblages on 31 land-bridge islands for two years in the Thousand Island Lake, China. Two frameworks were used to separate beta diversity (βcc or βjac) of each group into either species replacement (β-3) and richness difference (βrich) components, or turnover (βjtu) and nestedness-resultant (βjne) components. Mantel and partial Mantel tests were performed to determine correlations between pairwise dissimilarities and difference in island area, difference in distance to mainland and inter-island distance for each group. The multiple-island dissimilarity of spiders was primarily driven by turnover. Beta diversity (βcc or βjac) was positively associated with difference in island area in frequent ballooners, and negatively associated with difference in island area in occasional ballooners. Difference in island area had positive effects on βjne for all groups, but negative effects on β-3 and βjtu for occasional or non-ballooners. βrich was positively associated with difference in island area in frequent and non-ballooners. We did not find any significant isolation effects for these three measures of dissimilarity. The dominant process of extinction resulted in a high contribution of turnover to the multiple-island dissimilarity of spiders. Specifically, frequent ballooners contributed less turnover to multiple-island dissimilarity than occasional and non-ballooners. The most likely explanation for this is that frequent ballooners were potentially able to colonize all islands, whereas occasional and non-ballooners were constrained by water barriers and were unable to occupy most islands. Contrasting dissimilarities among dispersal groups of spiders demonstrates the importance of beta diversity partitioning, and the mechanistic insight gained on trait-dependence in community assembly.

Keywords: ballooning, beta diversity partitioning, dissimilarity, habitat fragmentation, spiders

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[*] Speaker

Phylogeography of coronavirus in bats in the Western Indian Ocean

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Bats are recognized as major reservoir hosts of emerging infectious agents. Coronavirus (CoV) have been reported in a large diversity of bat species, worldwide, and have been responsible of major outbreaks in humans, including the Severe Acute Respiratory Syndrome and the Middle-East Respiratory Syndrome. The South Western Indian Ocean (SWIO) region is an ecological system ideal for the study of the ecology and evolution of zoonotic viruses. This region is composed of continental islands separated from the African continent tens of millions years ago and oceanic islands that arose from the ocean between 1 to 15 million years ago, from volcanic activity. This complex geological history has shaped the colonization patterns of bats and their infectious agents. The goal of this study was to *(i)* estimate the prevalence of CoVs infection in bats in the western Indian ocean (Mozambique, Madagascar, Mayotte, Mauritius, Reunion Island, and the Seychelles), *(ii)* explore the genetic diversity of SWIO bat CoVs and *(iii)* identify potential association between bat families and CoVs genotypes. Based on 1114 sampled bats representing 40 species of 9 families (Emballonuridae, Hipposideridae, Miniopteridae, Molossidae, Nycteridae, Pteropodidae, Rhinolophidae, Rhinonycteridae, Vespertillionidae), we performed RNA extraction and RT-PCR on biological material (swabs and organs) followed by partial sequencing of the RNA-dependent RNA polymerase gene. A total of 88 bats (7.9 ± 1.6%) tested positive for CoV infection. A significant difference in the prevalence of positive samples was found between locations, bat families, and bat species. In particular, high prevalence of positive bats were found in Nycteridae (28.6 % ± 23.6%) and Rhinolophidae (24.6% ± 10.5%), and in Mozambique (19.6% ± 4.7%), as compared to bats sampled on islands. Phylogenetic analyses provided evidence that CoV positive bats harboured a large diversity of α- and β- coronaviruses, some being closely related to previously described human CoV. Also, we observed an association between bat families and CoV genotypes suggesting a long co-evolutionnary process.

Keywords: bats, coevolution, coronavirus, island biogeography, phylogeny

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[*] Speaker

The forgotten hotspot: a decade of research into the herpetofauna of the Comoros Archipelago

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The Comoros is an archipelago of four major oceanic islands in the Western Indian Ocean. Unlike Hawai'i, the Canaries, the Galápagos, and most other oceanic archipelagoes, the fauna of the Comoros remains poorly studied despite its high diversity and endemism. Today, reptiles may be the best-studied animal group of the Comoros. Reviewing my work of the last decade, I highlight the various biogeographic connections of the archipelago and the different colonization mechanisms of the past. Most reptile clades colonized the Comoros from the Northern tip of Madagascar, where the fast-flowing North-East Madagascar Current acts as an overseas dispersal 'conveyor'. The ancestors of other species of reptiles colonized the Comoros from central western Madagascar, continental Africa, or the Eastern Indian Ocean. In addition to common intra-archipelago dispersal and speciation, I present possible evidence of several extinction events followed by, or following, (re-)colonization by closely related lineages from Madagascar. In the *Ebenavia inunguis* species complex of geckos, the clade inhabiting the three western islands of the Comoros is sister to all other extant lineages. Its estimated age is substantially older than the extant islands of the archipelago (13–20 vs. ca. 11 million years). Furthermore, the two species of frogs from the Comoros are among the comparatively few unambiguous examples of amphibian species endemic to oceanic islands. Finally, I present recent advances in species conservation and the results of an atlas of the distribution of the reptiles and amphibians of the Comoros Archipelago.

Keywords: amphibians, atlas, biogeography, overseas dispersal, taxonomy, reptiles

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*Speaker

The role of ecological specialization in patterns of insular communities

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The dominant models in island biogeography implicitly treat all species as ecologically equivalent, especially when addressing effects of area, environmental heterogeneity and/or other factors on species richness. Some authors have attempted to treat generalist and specialist species separately or to use such a distinction in explanations of phenomena like the Small Island Effect (SIE). Nevertheless, previous approaches have kept the respective characterization binary, classifying species in one or the other category. Species, though, occupy a different position within the generalist-specialist continuum and this diversity of ecological roles might have important consequences for patterns at the community and meta-community levels. In the present work, we explore the effects of area and environmental heterogeneity on a modified metric of species richness that incorporates the varying ecological specialization of different species. We used a data set with terrestrial isopods from Aegean islands (Greece), for which a detailed description of each species' habitat exploitation range was available. We replaced the mere presence of each species in the presence/absence matrix with the number of habitat types it exploits in the study system and, for each island, we estimated an index of 'ecorichness', as the sum of these values for all its species, standardized with its total number of species (to control for variation in species richness among islands). Then, we explored the relation of this index with area, habitat diversity and the 'Choros' model. We tested significance of results using a null model approach, by drawing 'ecorichness values' from a randomized species pool with either the same distribution of ecorichness values with that of the observed matrix or a different distribution, such as normal or negative binomial. Our findings reveal radically different responses of small and large islands, documenting the increased role of ecological specialization with area. Given that habitat diversity of the studied system does not show 'saturation' with area, our results can be explained only by the increasing contribution of specialists that is in agreement with previous hypotheses on the processes leading to the SIE and with the role of habitat diversity in the shaping of insular communities.

Keywords: species area relationships, generalists, specialists continuum, habitat diversity, Choros model, island biogeography, Aegean archipelago

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Systems, landscapes and vegetation of the Iles Eparses (South-West Indian Ocean): geobotanical survey of Europa island

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The Iles Eparses comprise four low altitude (4-14 m) coral islands with terrestrial habitats located in the South-West of the Indian Ocean, close to Madagascar : Europa, Juan de Nova and the Iles Glorieuses in the Mozambique channel, and Tromelin in the North of the Mascarene archipelago. Between 22◦ and 11◦ South, the Iles Eparses fall into a south/north climatic gradient spanning from a semi-arid climate (Europa) to a more humid climate for the most northern island (Glorieuses). They administratively belong to the 5th district of the French Southern and Antarctic Land, a French Oversea Territory, since 2007. In spite of their reduced terrestrial area (from 30 km2 for Europa to 1 km2 for Tromelin), these islands share an exceptional natural heritage including many marine and terrestrial endemic species. At a regional scale the Iles Eparses are some of the most pristine ecosystems, largely preserved from anthropogenic impacts due to their geographical isolation and a historically very limited human occupation. In parallel with an updated account of the vascular flora published in 2018, a multiscale analysis of vegetation and plant landscapes was conducted according to the methods of geobotany including dynamic-catenal phytosociology, bioclimatology, geomorphology, and edaphology. Bioclimates have been established thanks to the four meteorological stations located on each of the islands. More than 1000 phytosociological surveys, mostly associated with geomorphological and ecological toposéquences, were carried out from 2004 to 2019. For each island, several typologies have been established: vegetation, series and systems of vegetation. Using the the colorimetric analysis and image segmentation method developed by IGN in the french national habitat mapping program (CarHAB), a map of vegetation systems has been drawn up for each island. We present here the first geobotanical survey established for the island of Europa. This atoll south of the Mozambique Channel has suffered little human disturbance, these remaining sectorized to a small part of the island. For the rest, the island is an exceptional place for the study of catenal structure and vegetation dynamics in response to marine and terrestrial ecological gradients and natural cyclonic, marine and avifaunistic disturbances.

Keywords: coral islands, geobotany, vegetation, vegetation mapping

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Why theory in island biogeography needs to integrate within-island heterogeneity and non-neutral species

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Most established theories in island biogeography are neutral as all species are treated equally and each island is integrated as one unit. MacArthur & Wilson already acknowledged this unrealistic aspect of their theory in 1967. However, it is only now that trait availability and computational power allow testing species pool concepts that account for species-specific differences. In addition, as potential island colonisers vary in their adaptation to environmental conditions, different ecozones within islands should differ in establishment probabilities of focal species. The objective of this talk is to outline the potential of a non-neutral theory of island biogeography. Using dispersal and plant growth strategy related trait patterns within islands I will show that ecozones within islands can be quantified as distinct biogeographical units. The evolutionary dynamics within the island should be influenced by these differences. Analyses of the distribution pattern of endemic species within islands provide strong support for this expectation. Further highlighting the potential of within-island studies, I will use the convergent evolution of secondary woodiness to show that the differences in environmental conditions within islands can be used to test fundamental questions in biogeography. Integrating within-island heterogeneity into theories in island biogeography is thus a crucial step forward.

Keywords: dispersal, island biogeography, plant growth stategies, secondary insular woodiness, theories in island biogeography

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An extended framework for the general dynamic theory of biogeography

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The General Dynamic Model of biodiversity (GDM) explains patterns of species richness on volcanic hotspot archipelagos with respect to island age (T) and area (A) by adjoining a hump-shaped function of T to the species area relationship (SAR). There are three main GDM models: 1) the semi-log ATTˆ2 model, which is an extension of a semi-log SAR, 2) the Power ATTˆ2 model which is a linear combination of a quadratic expression of island age and power law SAR and 3) the LogATTˆ2 model, where a power law in A is scaled by a lognormal function of T. We assess the relative performance of these models and compare their performance to other models including A or T or both. In light of our findings and the mathematical properties of the best performing models, we propose an extended framework for species richness models within the GDM. Species richness data was gathered from databases and published sources, resulting in 30 datasets for various taxa. We used the Akaike Information Criterion corrected for small sample size (AICc) to compare the relative performance of all models tested. Of the GDM models the LogATTˆ2model performed best in all cases. However, in almost 3/4 of the cases the best model overall was one that contained A or T only. For the Canary Islands area was not a significant predictor for any taxa which was probably due to the two old, low lying, but still relatively large islands of Fuerteventura and Lanzarote. The mathematical properties of the Log ATTˆ2 can be leveraged to derive an extended framework within the GDM which both connects it logically to other models and incorporates the cases where models containing only A or T were the best models. It also allows one to formulate a criterion for the consistent inclusion of predictors other than A and T i.e., that a substituted variable (say, elevation or a habitat diversity measure substituted for area) or an adjusted variable (say, area adjusted by an aridity index) have an approximately lognormal profile in T.

Keywords: general dynamic model, species area relationships, species richness, island ontogeny, choros model

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Effects of current and historical geography on island biodiversity revealed by an agent-based computer simulation

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Oceanic islands continue to pose intriguing study questions, and tools from computer science allow us to approach these classical systems in a novel way. Mechanistic simulations enable researchers to experiment and test theories at large spatial and temporal scale, and thus, can greatly help us to understand the processes behind island biodiversity patterns. We have developed an agent-based computer simulation to study the effects of habitat diversity, archipelago configuration and geological history of Hawaii, Galapagos, Canary Islands, Cape Verde and Azores. Our simulation is spatially explicit, non-neutral and emulates real-world archipelagos, which is a rare combination in island models. We used simplified archipelago maps as a simulation arena and implemented immigration, dispersal, establishment, competition, evolution and disturbance on autonomous agents, which represented populations of different species. We tested how habitat diversity and spatial configuration of archipelagos affected the correlations between simulated and observed plant diversity. We also tested for effects of the geologic history of Hawaii, Galapagos and the Canary Islandson plant, bird and insect biotas. We ran three scenarios for each archipelago: with a static present-day map, with a static Last Glacial Maximum map and with a dynamic map in which island properties changed, mimicking island growth and erosion. We found habitat diversity to be an important factor to achieve realistic simulation results in all five archipelagos, whereas archipelago configuration was important only in the archipelagos with more linear configuration (i.e. Hawaii and Azores). Results also suggest that Last Glacial Maximum geography and geologic history have had a strong effect on plant and insect biodiversity in Hawaii and Galapagos, but less so in the Canary Islands. For birds, we found a universal trend across all archipelagos: present-day geography led to the most realistic simulation results, suggesting that birds as a very dispersive group have already adjusted to the present archipelago geography. The emergent patterns from our simulations suggest that both current and historical geography affect the biodiversity of oceanic archipelagos and that the effects differ among archipelagos and taxonomic groups. We suggest that agent-based simulations are an effective yet underexplored tool for gaining mechanistic knowledge of island biodiversity.

Keywords: habitat diversity, archipelago configuration, geologic history, agent based simulations, computer simulations

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The small island effect: an appraisal of mechanisms

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The small island effect (SIE) can be broadly described as a different relationship between island area species richness on smaller islands compared to larger ones. The first graphical representation of the pattern was in 1963, and the SIE has been the subject of widespread renewed interest over the last 15 years. However, there is still considerable debate surrounding the mechanisms underpinning the pattern. In this regard, a number of mechanisms have been argued to underpin the prevalence of SIEs in island systems, and these can be broadly split into two groups: 1) mechanisms based on the idea that on small islands extinction rates vary independently of island area, and 2) mechanisms focused on a primary role for habitat diversity in driving the SIE. However, these different mechanisms have been studied in isolation and we lack a clear understanding of their relative importance. Here, we focus on a large and well sampled dataset of plant species distributed across multiple islands of varying size in the Aegean Sea. First, we compiled a database of the presence-absence of 3262 native plant species on 173 Aegean islands. We then compared piecewise regression models with standard linear SAR models to assess whether there was a breakpoint in the SAR (i.e. a traditional SIE). After finding strong statistical support for the presence of a SIE in the data, we used information on island characteristics and the evolutionary relationships between species to undertake an extensive evaluation of the mechanisms driving the observed SIE. Our findings provide evidence supporting the role of habitat diversity in driving the traditional SIE, and thus improves our understanding of community assembly on islands more generally.

Keywords: small island effect, species, area relationship, thresholds, island biogeography

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Isolation by elevation promotes speciation on islands globally

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Islands and elevational gradients provide valuable opportunities for testing hypotheses to explain diversity gradients. One such hypothesis, which has received recent support from a global study of islands, is that isolation from equivalent climates increases per-species speciation rate. Higher-elevation areas on islands and continental mountains tend to be separated by longer distances from equivalent climates, predicting higher speciation rate and endemism at higher elevations. So far, this has only been tested for archipelago-level isolation and endemism. Here we test novel predictions derived from the hypothesis, for island plants: single-island endemics are correlated only with within-archipelago elevational isolation (prediction 1); multi-island endemics are correlated more strongly with extra-archipelago elevational isolation (prediction 2). Using 100 m elevational bands and entire floras for each of 32 high-elevation islands, we calculated the proportion of native species that are (i) single-island endemics, (ii) multi-island endemics and (iii) archipelago endemics. We tested their correlations with the different measures of elevational isolation. The results were consistent with both predictions: the percentage of single-island endemics correlates with isolation from the next island, while the percentage of archipelago endemics correlates with isolation from the mainland. This may represent an important step forward in understanding island endemism, and patterns of biodiversity more generally.

Keywords: Archipelago, elevational gradients, endemism, isolation, speciation

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[*] Speaker

The role of habitat heterogeneity in the taxonomic and functional diversity of Macaronesian spider communities

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Despite the fact that we have improved our understanding of how island age, size and isolation affect the structure of insular communities, we still fall short in knowing the effects of environmental (climatic and (micro)habitat) variability on the diversity and functional structure of island communities at different spatial scales, i.e., from small plots, to habitats, islands and archipelagos. In this work we use the Macaronesian archipelagos as a model to understand the effects of environmental heterogeneity on the taxonomic and functional diversity of spider communities. By using standardised data from across four archipelagos with a range of climatic and (micro)habitat conditions, we tested two hypotheses related to the consequences of environmental heterogeneity: 1) variation in spider communities responds positively to heterogeneity at both regional and local plot scales; and 2) local environmental conditions act as a second functional filter for species into the communities that they ultimately form. Following the standardised sampling protocol COBRA, we collected spider specimens at 50 m x 50 m plots across eight Macaronesian islands. We generated community data from taxonomically identified and functionally characterised specimens and species, and obtained climatic and habitat data from satellite imagery. Through a series of null-models and hierarchical linear models, we tested the relationships between environmental variability and alpha and beta diversity for several functional groups. Habitat type, and environmental and (micro)habitat variability were correlated, with dry habitats having more heterogeneous climates and habitats. Spider communities were also more variable (greater beta diversity values)

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at both regional and local scales. The response of the functional structure of spider communities to environmental variability was reflected in the differences in the relative abundances of species belonging to different predatory guilds: web building species were more dominant in structurally more complex areas. Our findings point at the need to consider different spatial scales when investigating the effect of environmental heterogeneity on the assembly and structure of island communities.

Keywords: macroecology, Macaronesia, spider Communities, functional diversity, habitat structure

A roadmap for island bryophyte biogeography and evolution

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In the last years we have seen a fascinating progression in the knowledge of how evolutionary and ecological processes shape biodiversity on islands, but also how insular biotas interact with continental biological assemblages. However, distinguishing among processes that can take place over different timescales but causing similar (phylo-)genetic signatures has remained problematic. In this respect, cutting-edge analytical tools have brought unprecedented insights into the mechanisms governing community assemblage on islands. The same technical advances have challenged the view of oceanic islands as evolutionary dead-ends, which had been built on typical insular syndromes such as the loss of dispersal capacities, to recently emphasize the role of oceanic islands not only as hotspots of endemism but also as glacial refugia for continental biodiversity. Here I review whether traditional theories in biogeography and evolution hold for extremely mobile organisms, using bryophyte floras from oceanic archipelagos as a model. In particular, I revisit questions such as (i) how oceanic island and continental bryophyte floras relate; (ii) to what extent the island syndromes apply to this group of spore-producing plants; and (iii) what mechanisms or phenomena can explain the low levels of island endemism observed in bryophytes as compared to angiosperms. Based on innovative biogeographical, phylogeographic and genetic approaches, this talk aims at providing a general view on the underlying processes that shape diversity and community assembly in bryophytes, opening the door to exciting avenues of research.

Keywords: diversification, diversity, long distance dispersal, oceanic islands, speciation

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*Speaker

Distribution and relative age of endemism across islands worldwide

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Islands are recognized by their remarkable rates of endemism so highly contributing to global diversity. One point remaining to be explored is the age of island endemics as it may provide new insights on the processes at the origin of island biota. We studied this issue by investigating the relative age of Monocots in islands worldwide,employing a measure of phylogenetic endemism and a method based on null models. We used the most comprehensive dataset on species occurrences in 4,306 islands, and identified 142 sites with neo-, paleo-, mixed and super-endemism. They were distributed all over the world, but more common at low latitudes. Mixed and super-endemism were the more frequent, putting in evidence the commonness of processes at all time scales at shaping present island biodiversity. Especially, we showed the importance of latitude, habitat availability and climate stability on the persistence of ancient taxa and on recent diversification events. These findings represent a great contribution to guide biodiversity conservation at global scale. These islands are irreplaceable both for the uniqueness and evolutionary history of their flora, so highly contributing to preserve "option values" and evolutionary potential.

Keywords: Global scale, paleo endemism, neo endemism, mixed super endemism, phylogenetic endemism, evolutionary potential

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The Pacific basin as a laboratory to study islands disharmony

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Biogeographers and naturalists have long observed and documented disharmony in islands, i.e. the compositional distinctiveness of islands compared to the mainland, but the first quantification of this concept is only very recent. A previous study on the world's island floras showed a mixed effect of dispersal and environmental and biotic filtering, presenting disharmony as a useful entry point to understand the structure of island assemblages. In our study, we used the Pacific basin as a study system to test, at fine spatial grain, how the processes of dispersal and environmental and biotic filtering can result in disharmony in island faunas. We measured the diversity and proportion of families within the terrestrial orders of mammals, birds, and amphibians from their distribution ranges. The Pacific basin, bounded by continental margins, can bring new insights into disharmony because of the high diversity of geological and geomorphological attributes of its 1179 islands, and their complex history of dispersal events. This complex spatial matrix requires a robust statistical framework to disentangle the potential confounding spatial effects in the study area, the island characteristics, and the potential species pools. The first results of the models show how different potential source regions can shed light on the processes resulting in disharmony. Our work provides a contribution to a better understanding of spatial effects on disharmony.

Keywords: disharmony, Pacific, species pool, terrestrial

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Do endemic trees flora make endemic forests? Insights from New Caledonian forests

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New Caledonia homes a rich and highly original flora with a species endemic rate > 75% and fascinating representation of relict taxa (gymnosperms and basal angiosperms). As a result, previous studies on the island flora have mostly focused on the taxonomy and biogeographical origins of this exceptional flora while few studies have attempted to understand the spatial distribution of species and the structure and diversity of species assemblages. Here, we present new insights into the diversity, structure, and ecology of trees communities derived from the New Caledonian Plant Inventory and Permanent Plot Network (NC-PIPPN). NC-PIPPN consists of standardized forest inventories scattered throughout the New Caledonian main island. This network groups together ca. 450 plots including more than 70 000 occurrences of woody plants (trees, shrubs, lianas, tree ferns, and palms) belonging to more than 950 mostly endemics species. Most species are distributed along wide environmental ranges (ca. 900 m of elevation and 2200 mm of mean annual rainfall) and contrasted substrates (volcano-sedimentary, ultramafics and calcareous). Wide environmental ranges, however, do not significantly correlate with large spatial distribution or high local abundance. As in other places in the tropics, the diversity of the forests is support by a highly uneven species abundance distribution. Less than 20% of tree species account for > 50% of all known occurrences, while half of the tree species contribute to < 16% of occurrences. Local abundance is also independant to spatial distribution: some rare species at the island scale are locally abundant while some frequent species at the island scale are locally rare. The spatial distribution of species results in highly heterogeneous forests (high beta diversity) that contrasts with a relatively homogeneous structure of communities. Despite a highly original flora and a pattern of aggregative species distribution, New Caledonian forests are not so distinguishable from other forests in the South Pacific region. Our results suggest that the New Caledonian rainforests are mostly constrained by geographical features (area and isolation of the archipelago) and climatic features (e.g. cyclonic frequency) while the flora uniqueness poorly contribute to the forest structure.

Keywords: New Caledonia, diversity, communities, trees

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Understanding patterns of micro-endemism in chameleons: case of *Furcifer nicosiai* (Reptilia, Chamaeleonidae) in the western dry forest of Madagascar

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In Madagascar, although chameleons in the genus *Furcifer* are considered as generalists and widely distributed, a few species occur in small geographic areas. Factors leading to such micro-endemism have been studied for the genus *Brookesia* but not for *Furcifer*. This study is an attempt to understand the distribution pattern of an endangered and micro-endemic species, *Furcifer nicosiai*, in the dry forests of western central Madagascar. Available literature about this species, including its distribution, ecology and phylogenetic relationships with other members of the genus, was reviewed. Additional ecological data on habitat and perch use were collected in the regional forests. The species is currently known in the protected areas of Bemaraha and Menabe Antimena. The results indicate that climate is a major factor influencing the distribution of *F. nicosiai* rather than soil substrate. This species is unknown beyond the northern part of Bemaraha, where there is increased humidity, or below the southern portions of the Menabe Antimena forests, where there is a decrease in rainfall. Even though Bemaraha and Menabe Antimena are separated by two major rivers (Manambolo and Tsiribina), these potential barriers have not limited dispersal. Based on preliminary survey data, *F. nicosiai* is unknown to occur in the Masoarivo forest blocks between the Manambolo and Tsirabihina Rivers. Two hypotheses can be advanced: 1) during a period of range expansion, *F. nicosiai* only used the region of the existing Masoarivo forest as a dispersal corridor without establishing a population in this area or 2) the local Masoarivo population was subsequently extirpated associated with human-induced degradation of this forested zone. Further, the habitat and perch use of *F. nicosiai* showed a preference for more open forested habitats in largely intact areas, with trees and shrubs of less than 8 m high and 2.5 cm dbh. As these results highlight the apparent specificity of this species regarding microclimate and presumably habitat loss, conservation actions need to be reinforced in the area containing the known distribution of this species. Moreover, additional fieldwork needs to be conducted in the relict Masoarivo forests to verify its absence from this zone.

Keywords: Bemaraha, dispersal, Furcifer nicosiai, Menabe Antimena, protected areas

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[*] Speaker

Out of the blue – the phylogeographic tale of freshwater amphipods (Malacostraca) from the Mediterranean Islands

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Malacostraca is a highly diversified and very speciose class of crustaceans. Out of the estimated 26,000 malacostracan species described so far, about 6,000 inhabit various freshwater habitats worldwide. The Mediterranean region has been recognized as one of the 25 most important biodiversity and endemism hotspots worldwide and its islands are considered to be the natural laboratories of the evolution. Even though, the Mediterranean region is housing roughly 6% of world freshwater taxa, the knowledge about the freshwater fauna of the Mediterranean basin is incomplete and the studies upon the freshwater biota on the Mediterranean Islands very scarce. The majority of the insular freshwater malacostracans is comprised of amphipods. In particular, family Gammaridae is known to be a major component of the epigean freshwater communities, playing a key trophic role in the freshwater communities in the Mediterranean Region. More than 600 individuals from nearly 150 sites from the Mediterranean Region were amplified for several mitochondrial and nuclear markers, which revealed an extraordinary level of yet undiscovered biodiversity with more than 50 distinct entities, tripling the number of currently described insular species. The reconstruction of time-calibrated phylogeny have supported the assumption that the evolution of the freshwater gammarid amphipods is strongly connected with the geological history of the region with many lineages present on the islands already for millions of years. Our studies on various islands like Sicily, Crete, Sardinia, Mallorca and Aegean islands, confirmed high level of overlooked diversity in the insular fresh waters. Given that the Mediterranean Islands are housing more than 25% of freshwater malacostracans of the entire Mediterranean Region, with more than a half of them being insular endemics and considering that the ongoing climate change and heavy anthropogenic activities makes the freshwater ecosystems the most vulnerable and prone to mass extinctions, we point out that there is an urgent need for raising the public awareness about the level of insular freshwater biodiversity, which should be one of the focal points of the island biology.

Keywords: Mediterranean islands, freshwater, Amphipoda, Malacostraca, Crustacea

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*Speaker

Changes in biota following volcanic eruption on Nishinoshima island among the Ogasawara islands in subtropical Japan

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Nishinoshima is a volcanic island among the Ogasawara Islands of subtropical Japan. In November 2013, a major eruption began on this island; continuing intermittent eruptions covered nearly the entire island with lava flows. These lava flows formed new land, increasing the area of the island from 27 to 295 ha. Before the 2013 eruption, six plant species and eight breeding seabird species were found on the island; however, their habitats were almost completely destroyed by lava flow. To estimate the impact of the eruption, I investigated floral and avifaunal changes using a land survey and aerial photography. In 2016, three plant species and three breeding seabirds were confirmed to have survived the 2013 eruption. By 2018, another three breeding seabirds were found. Plant distribution was limited to on and around a small remnant of the former island, although it recovered to some extent between 2016 and 2018. Seabird responses to the event differed among species, with some seabirds using the newly formed land for breeding. In particular, the breeding range of the brown booby *Sula leucogaster*expanded significantly, regaining its pre-eruption population size. Increases in population sizes among the masked booby (*Sula dactylatra*)and greater crested tern (*Sterna bergii*) are now greater than before the eruption, whereas those of the wedge-tailed shearwater (*Puffinus pacificus*) and brown noddy (*Anous stolidus*) have decreased. Although the eruption had a devastating impact on the biota of the island, some seabirds benefited from the expansion of land area and increased habitat diversity. Future monitoring of the changing biota on the new-formed land would provide empirical knowledge of species assembly on these isolated oceanic islands.

Keywords: volcano, eruption, avifauna

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*Speaker

Islands in the ice: patterns in and threats to the unique terrestrial biodiversity of the Antarctic

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Antarctica may not conjure up pictures of islands, although clearly this description applies well to the remote sub-Antarctic and Southern Ocean islands. However, its terrestrial biodiversity is in large part restricted to tiny islands of ice-free habitat surrounded by vast expanses of inhospitable ice. Recent advances in understanding of Antarctica's terrestrial diversity have emphasised that it is characterised by much stronger regionalisation and palaeoendemism than previously suspected. In an era of recent and predicted future regional climate change, this generates important new threats to the native biodiversity of the ice-fee 'islands' of this still largely pristine continent. This presentation will briefly introduce the form, distribution and regionalisation of terrestrial diversity within and around Antarctica, along with recent modelling studies of future climate, and the effects this will have on the distribution and extent of ice-free ground, and the distribution of both native and non-native biota. The potential role of direct human activity as a driver of changing distributions will be emphasised. The study integrates the outcomes of recent research modelling current and future native and non-native species distributions in Antarctica with published models of future predicted climatic changes and associated changes in the extent of ice-free ground. The intensity of human activity providing linkages between otherwise biogeographically isolated regions is also superimposed to identify areas at particular risk of human-assisted biological invasions. Focusing on the Antarctic Peninsula region, the decades to the end of the 21st Century will see a rapid increase in the extent of ice-free ground, but the coalescing of currently isolated areas increases the risks of genetic diversity loss through homogenisation. Rapid southwards movement of both native and current and future invasive species is likely due to increasing environmental suitability. Some distinct biogeographic regions of the Antarctic Peninsula and continental coastline have overall sufficiently similar climates that human connectivity between them risks facilitating the inadvertent movement and establishment of biota. The study emphasises the urgent need for establishment of robust and practical biosecurity measures for both entry to and movement within the Antarctic region, backed by strong survey and monitoring effort.

Keywords: bioregionalisation, climate change, distribution modelling, connectivity, invasions, human assistance

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*Speaker

Distribution of genetic diversity of the subantarctic crab *Halicarcinus planatus*: first marine alien reaching Antarctica

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Antarctica remains the most pristine and isolated continent on earth, surrounded by oceanographic, bathymetric, geographic and climatic barriers. Nevertheless the latter is being softened by the global warming, which is especially strong on the West Antarctic Peninsula. This warming enhances the probabilities of introduction of subantarctic alien species, and their subsequent proliferation. Shallow marine benthic communities around Antarctica exhibit high levels of endemism, gigantism, slow growth, longevity and late maturity. Several families of durophagous predators that are highly abundant and diverse in subantarctic shallow waters are almost completely absent in the Southern Ocean, this is the case of decapods. In 2015, a breeding female *Halicarcinus planatus* was reported in Deception Island (South Shetlands, West Antarctic Peninsula). This s pecies is a brachyuran crab with a circum-subantarctic distribution. *Halicarcinus planatus* has a low bathymetric range, a planktonic larval duration of 45-60 days, and unlike other decapods, it tolerates temperatures near 0◦C. This crab is able to reduce the magnesium concentration in its haemolymph that increases with the cold. The present project evaluates the level of genetic diversity of *Halicarcinus planatus* along in southern South-America as well as in Subantarctic Islands, determinates the phylogeographic structure of the species, the geographic scale at which the genetic differentiation operates and the connectivity pattern between remote island populations such as those from Falkland/Malvinas and Kerguelen Islands. The phylogenetic relationships are inferred from mitochondrial and nuclear haplotypes from the Magellanic Region, Falklands/Malvinas and Kerguelen Islands. The levels of diversity of *Halicarcinus planatus* populations are the highest in southern South-America, but tend to decrease toward the north, whereas in Subantarctic Islands they are significantly lower. The mitochondrial haplotype network is dense and strongly reticulated, showing no sign of population-size reduction in Patagonia. The phylogeographic relationships across the Southern Ocean indicate than the the species originally expanded it range in the Patagonia and dispersed to Falkland and Kerguelen Islands by long distance dispersal.

Keywords: circumpolar current, Falkland/Malvinas, Kerguelen, long distance dispersal, phylogeography

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Biological Invasions on Islands

Contents

New insights on the origin and dispersion history of invasive populations of the small Indian mongoose, *Urva auropunctata*, in the Caribbean islands

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Invasive alien species (IAS) represent one of the major factors of erosion of global biodiversity, especially within island environments. The study of the dynamics of introduction and dispersion of IAS is therefore at the heart of conservation efforts in insular ecosystems. The small Indian mongoose, *Urva auropunctata*, is a carnivore whose native range extends from Middle-East countries, to northern India, Nepal and Myanmar. However, the species was introduced into a large number of islands of the Pacific and Indian Ocean, as well as islands of the Adriatic and Caribbean seas during the 19th and 20th centuries. This work was conducted with the aim of understanding the origin and dispersion of the populations of small Indian mongooses in the Caribbean. In addition to the sequencing of two mitochondrial markers (Cytochrome b and Control Region) from 129 samples of native and introduced zones, we developed 23 new microsatellites markers to genotype 480 individuals from six Caribbean islands, including some populations never sampled before. Classical descriptive statistics as well as spatial approaches were used to infer genetic structure patterns and colonization dynamics. Both mitochondrial and microsatellite markers revealed a strong structuration of the Caribbean populations into two main groups: the first includes the populations of Jamaica, Puerto Rico, Saint Kitts, Saint Martin, the Virgin Islands, and Grenada; the second grouped the populations from Guadeloupe and Martinique. Jamaica had the highest number of haplotypes, unique or shared with the several islands mentioned above. This results suggests, consistently with the historical records, that Jamaica could be the local source of the introduction to the other Caribbean islands formerly part of the British West Indies. These data also suggest that the populations from Jamaica originated from Southeast India or Bangladesh, while the populations of Guadeloupe and Martinique appeared closer to Pakistan individuals, and therefore seemed to result from a different introduction. The genetic structure observed for the small Indian mongoose in the Caribbean islands reveals that introduction events reflects historical geopolitic relationships of the former colonies. Understanding these patterns as well as local dynamics should help improving pest management in this region.

Keywords: invasive species, *Urva auropunctata*, dispersion, Caribbean, genetic markers

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*Speaker

Invasive predator ecology and impacts in a biodiversity hotspot. The feral cat *Felis catus* in the New-Caledonian archipelago

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Feral cat (*Felis catus*) is one of the most successful and harmful invasive predator species for island biodiversity. The presence of this alien predator species generally lead to dramatic loss of native island biodiversity and represents a serious threat for numerous endemic and threatened species. Feral cats have invaded the whole New-Caledonian archipelago and all its habitats. In this study, we focused on the ecology and impacts of this invasive predator on the outstanding endemic fauna found in the different habitats of the exceptional New-Caledonia biodiversity hotspot. Feral cat diet analyses on 14 selected sites representing the 4 main natural habitats revealed a high diversified diet and high predation rates on native species particularly on squamates, flying foxes and petrels. Among the 44 vertebrates species found into the feral cat diet, 20 are IUCN red-listed threatened species. Cat movements of eleven feral cats fitted with GPS collars have been studied in a western coast Peninsula hosting an important seabird colony. Male cats showed large home ranges while female showed small home ranges. Feral cats exhibited important movements within the studied peninsula linked with the breeding cycles of seabirds. GPS data coupled with dietary informations suggested a predation that concerned both breeding adults and fledgings bird, and at a large geographic scale as some feral cats have their core home range distant to the colony (> 3km). We evaluated the effects of a high level but intense cat control on this site that showed a low sustainability of feral cat culling and a rapid recolonization process. Our results are pleading for the future limitation of feral cat impacts and call to focus first abundance limitation measures on maquis mosaic and humid forest habitats This study also provided information on the spatial extent and intensity of future control measures in the special context of a large and highly invaded island.

Keywords: biological invasions, islands, predation, movement analysis, predator management

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*Speaker

Is reproductive ecology behind the success of an invasive snake on a Mediterranean island?

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In 2003, three snake species native to the South Iberian Peninsula, entered Ibiza Island for the first time. Since its arrival 15 years ago, *Hemorrhois hippocrepis*, the Horseshoe Whip Snake, has continued to thrive well on the island and poses a threat to the endemic Ibiza Wall Lizard, *Podarcis pityusensis*, and potentially to 9 bat species and 57 bird species, all native and some of them listed as threatened. Here, we analyze its reproductive ecology to unravel whether it may be behind its invasive success. Particularly, we studied 545 specimens from the invasive population (224 females, 261 males and 60 immatures) and analyzed sexual dimorphism, body size at maturity, reproductive cycle, fat-body levels of both sexes, clutch size, newborn characteristics (size, sex ratio and weight) and female reproduction frequency of the Ibizan population, comparing these traits to those exhibited by the source population, on the south of the Iberian Peninsula. Surprisingly, Ibizan invasive Horseshoe Whip snakes are less efficient in general than those from the source population regarding this key aspect of its natural history, the reproduction. The size at maturity is rather similar between populations, with some invasive females maturing at smaller sizes than those from the source population. The reproductive cycle in both sexes is essentially similar between populations, perhaps with a temporal extension in the invasive population (earlier spermatogenesis and vitellogenesis). However, albeit the higher lipid reserves of the Ibizan snakes, more allochthonous than autochthonous females skip opportunities to breed in sequential years, and the same for some males, the latter unseen in the source population. Moreover, in spite of the larger body size of invasive females, they do not have larger clutch sizes than individuals of the source population. We conclude that reproductive ecology is not responsible for the success of the invasive population, leaving only one explanation, after having also studied its diet and predation pressure: the enemy release hypothesis.

Keywords: Ibiza, invasive species, Hemorrhois hippocrepis, Podarcis pityusenis, reproduction

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[*] Speaker

Twenty years of the invasion of the California kingsnake (*Lampropeltis californiae*) in Gran Canaria island

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The ecological and socioeconomic effects of invasive snakes are known to have been devasting on several islands worldwide. Although some cases are very well-documented (e.g. the brown tree snake on Guam), some others are relatively unknown. With this contribution we aim to update the current state-of-the-art regarding the invasion by the California kingsnake (*Lampropeltis californiae*, Colubridae) on the island of Gran Canaria (Canary Islands, Spain). We provide data on the past and current distribution, trophic ecology, and impacts of this species, which have been collected during the accomplishment of several projects in the last 10 years. The distribution of the species has been assessed with the participation of citizens, diet was studied by analysing the stomach and gut content of 1129 specimens. Impacts upon the endemic giant lizard have been quantified by censusing lizards through different methodologies in invaded and non-invaded areas. The California kingsnake was first detected in 1998 on the island. In 2007, when it was considered naturalized, there was only one population nucleus located in the east of the island. In 2010 a second genetically different population was found in the northwest of the island. Currently, four invasion foci have been found, with dozens of isolated individuals throughout the rest of the island. A total of 5383 snakes have been captured on the island since 2011. Diet analyses show that these snakes mainly prey upon endemic herpetofauna, the Gran Canaria giant lizard being the main prey in the first stages of the invasion, followed by the Gran Canaria skink and Boettger's wall gecko. However, invasive rats and mice become more consumed in later stages of the snake invasion, as snakes are causing local extinction of endemic lizards. In the light of what has been described on other islands worldwide and what is happening on Gran Canaria, we urge that islands suffering from invasive snakes should establish closer research collaborations. This

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will allow joint investigation into new innovative measures and techniques to combat highly invasive species that are disturbing and ruining island ecosystems.

Keywords: California kingsnake, Gran Canaria, impacts, Lampropeltis californiae, trophic ecology

Invasion dynamics of an amphibian with frequent human-mediated translocations on the Andaman archipelago

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Island communities can be highly susceptible to invasions, but also provide unique opportunities to manage invasions. Post species introduction to islands, human-mediated translocations (HMT) can alter the course of invasions by accelerating invasive spread. Therefore, modelling of invading organisms requires accounting for HMT along with complexities in species demography, spatial context, and natural dispersal. We aim to disentangle these invasion dynamics for the Indian bullfrog, *Hoplobatrachus tigerinus*, on the Andaman archipelago (Bay of Bengal, India) to assess i) the effect of HMT on colonization rates, and ii) the efficacy of two potential management interventions in limiting invasive spread. We combined an age-structured demographic model allowing stage-based dispersal with a gravity model of human influence, in a spatially explicit modelling context. We parametrized the model using life-history and dispersal variables from *H. tigerinus* (or similar species), and remote-sensed variables describing spatial heterogeneity. The modelled invasion dynamics of *H. tigerinus* shows human influence can increase spread rates by a factor of three, as compared to invasion without human influence on spread. Such exacerbation of spread rates is driven by facilitation of both between and within island movements of *H. tigerinus* by humans. The model also predicted an overriding effect of HMTs on the origin of invasion. Of the two simulated management interventions, only constraining movement of *H. tigerinus* between islands was effective in limiting spread, but success was dependent on time elapsed since introduction. Based on model predictions, we find merit in recommending screening at points of entry (e. g. ports) for the hitherto uncolonized Baratang and Long Islands. Although the model provided insights into the human influence on invasive spread in an archipelago context, it did not perform optimally in estimating demographic dynamics and natural dispersal. We demonstrate the suitability of this modelling approach in understanding invasions with persisting human influence, especially in island systems.

Keywords: island invasive, Hoplobatrachus tigerinus, Indian bullfrog, management, invasive spread

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*Speaker

Global distributions of three highly invasive bird species under climate change

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The red-vented bulbul (*Pycnonotus cafer*), the common myna (*Acridotheres tristis*) and the red-whiskered bulbul (*Pycnonotus jocosus*) are passerine bird species native to the Indian subcontinent. All three species were transported widely during the early 1900s as caged birds for trade by Indian workers. They are now considered invasive – occupying diverse habitats, feeding on and damaging a wide range of fruit, and out-compete native fauna. Predicting the current potential global distribution of these species is important to help identify locations where introduction-prevention should be prioritized. Of equal importance is an assessment of how climate change might alter their potential invasive ranges. Here, we used presence data from both their native and alien ranges and eight species distribution model (SDM) algorithms to predict their potential current ranges. We then used five global circulation models and four representative concentration pathways to predict their potential future ranges under climate change. Our results suggest that there is considerable overlap in the potential climatically suitable ranges of the three species, with the common myna having the widest potential range. Many islands, and particularly Mayotte, Madagascar, and the Indian Ocean Islands, appear to be climatically suitable for invasion. Our future projections highlight three locations (Guinea gulf, South America, and Gulf of Mexico) that could be climatically suitable for further invasion by these invasive species and predict potential shifts in the distribution of alien populations in four main geographical areas (Middle East, Australia, and South Africa). We believe that application of SDMs for invasive bird species under climate change scenarios, as used here, can offer managers a useful tool to generate potential-range distribution maps to assess and compare invasion risk at both local and global scales.

Keywords: biological invasions, birds, climate, islands, species distribution modeling

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Varroa destructor invasion in the South West Indian Ocean islands and its mortality impacts on the endemic honeybee subspecies Apis mellifera unicolor in Madagascar, Mauritius and La Réunion

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Invasive species cause severe impacts on biodiversity losses, among them, emerging diseases caused by parasites are also considered as invasive species. *Varroa destructor* is an ectoparasite mite native from South-East Asia and has spread all over the world since the early 50's. The mite is considered as the main sanitary threat for honeybee health worldwide. This parasite was detected for the first time in the islands of the South-West Indian Ocean (SWIO): 2010 in Madagascar, 2014 in Mauritius and 2017 in La Réunion. The aims of this work were (i) to characterize the genetic diversity of the parasite on the three islands, (ii) to assess the mortalities within honeybee population after the detection of *V. destructor* and (iii) to assess the spread of the parasite and identify the associated drivers. To identify the parasite strain and its diversity, mitochondrial DNA sequences were analyzed. Sanitary and epidemiological surveys were conducted in Madagascar, Mauritius and La Réunion. The varroa strain identified in the SWIO area was the invasive K strain, nevertheless several haplotypes were retrieved, among which one was common in Madagascar, Mauritius and La Réunion. The parasite invsasion increased significantly the mortalities in the honeybee populations (for example, +185% of mortalities were observed in La Réunion). Beekeepers played a major role in dispersing the parasite within the islands and the dispersion speed estimated was higher in La Réunion and Mauritius than in Madagascar where the beekeeping practices are really different (modern vs. traditional). Varroa mite eradication cannot be an option for local beekeepers and several control options should be considered. Several other sanitary threats such as *Aethina tumida* (small hive beetle) and *Paenibacillus larvae* (American foulbrood) threaten the honeybees from the SWIO islands. In this insular context, routes of introduction have to be identified and the sanitary surveillance tools should be improved for all the islands.

Keywords: honeybee, invasion, mortalities, surveillance, SWIO, varroa destructor

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[*] Speaker

Towards island-specific scenarios of biological invasions in the 21st century

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Biological invasions have emerged as an eminent feature of recent global change, with substantial impacts on the environment and human livelihoods. Recent research demonstrated that numbers and impacts of alien species are rising unabatedly. At the same time, we lack a thorough understanding of potential future trajectories for the decades to come. With the recent establishment of comprehensive global databases on alien species distributions and impacts, it is for the first time feasible to develop and quantify future scenarios of biological invasions. Islands are especially interesting study systems as they host major biodiversity hotspots with exceptionally high endemic richness. However, anthropogenic pressures, like climate change, land use and land-cover change, pollution, overexploitation and invasive species increasingly threaten native island biodiversity. From a biological invasion perspective, islands host disproportionately high numbers of alien species compared to mainland regions and absolute numbers often exceed the native richness of flora and fauna. Further, invasive alien species are among the major threats for island biodiversity being involved in 86% of all recorded island extinctions. Here, we present a conceptual framework and a roadmap for the development of island-specific scenarios and models on how alien species richness and impact might change in the 21st century. This includes the establishment of qualitative scenario narratives and the quantification of pressures and impacts for these narratives. We aim at understanding the long-term trajectories of biological invasions on islands under different assumptions of the future, both qualitatively and quantitatively. Evaluating the option space for reducing the impacts of invasive species on island biota is crucial to develop adequate management and policy options. Finally, we aim to engage with the participants of the Island Biology Conference and utilize their expertise and wide variety of backgrounds to refine the central questions such scenarios should address.

Keywords: scenarios, storylines, predictions, impact, management, policy

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Community / Functional Ecology

Contents

Niches and neutrality on a tropical oceanic island: explaining diversity and turnover in moth assemblages in island rainforests

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Spatially driven turnover in species composition and relative abundance drives gamma diversity in all ecosystems. Assemblages of nocturnal Lepidoptera in rainforests are powerful tools for estimating and understanding this heterogeneity. There are three fundamental theoretical hypotheses for explaining this place-to-place change: neutral stochasticity, niche-driven opportunity and historical contingency. These mechanisms may act in concert and, in any case, are not necessarily independent of each other. At two seasons in 2018 we sampled moths across a set of ten sites in the mid-elevation rainforests of eastern Réunion. A total of 6115 individuals of about 280 species was processed. We analysed these against distance and pre-existing data on the woody flora of the same sites. Unique for these data sets, we were able to subdivide the species encountered into local and regional endemics, and non-endemics. The outcomes are complex but, in summary, local occurrence of the generally more diet-restricted endemic moths is more likely to be niche-driven due to evolved host-plant preferences while occurrence of the generally more polyphagous non-endemic species is most parsimoniously explained by stochastic neutral mechanisms. Spatial pattern in the underlying native flora may also occur as stochastic neutrally assembled sets across the rainforest region (with implications for native moth species) whereas introduced species reflect human-driven historical contingency. Implications of future changes will be discussed.

Keywords: Mascarenes, moths, Lepidoptera, Réunion, species turnover, woody plants

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Diversity and community composition of herbivorous thrips vary along environmental gradients, but plant effects remain an important driver

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Elevational gradients are a powerful tool to explore how species communities respond to changes in environmental conditions along short geographic distances. It is usually observed that species diversity decrease monotonically with elevation, or follow a mid-elevation peak. These effects, however, may vary among taxa and geographic regions. Changes driven by elevation may also depend on landscape characteristics like habitat heterogeneity and patchiness, but also on seasonal variations such as those occurring between cold and hot seasons. Here, we used as biological model thrips (Insecta: Thysanoptera), which is a diverse group of slender insects, to investigate the drivers of insect diversity and of community composition along elevational gradients in Reunion Island. We sampled thrips on 106 plant species belonging to 44 families along seven replicated elevated gradients from 0 to 1,600 m in both summer and winter conditions. We identified 4,278 specimens representing 41 species and we estimated their diversity both at the local (alpha) and at the compositional (beta) diversity level. These metrics were related with elevation, and with landscape characteristics around each site, which included habitat diversity and patchiness (or fragmentation). We found that different thrips communities are directly related to host plants: invasive plants hosted a large diversity of thrips, whereas some endemic ones hosted unique communities. Elevation, patchiness and season were variables with an evident effect on both alpha and beta diversity. Beta diversity revealed that diversity of thrips was larger at low elevations, and this change was mostly dominated by richness differences (i.e. low elevation sites had more unique species than high elevation ones). Our results show that important diversity patterns can be appreciated through the lens of beta diversity, and may help to understand how regional pools of insects are distributed in relationship with topography, landscape and climatic conditions.

Keywords: tropical island, environmental gradients, beta diversity, alpha diversity, thrips

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A trait-based approach to assess functional responses of epiphytic liverworts to environmental gradients

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Assessing species responses to changes in their environment and the effect of biotic interactions in shaping communities, are important steps in understanding ecosystem functioning. A trait-based approach assessing community diversity might be as important as, and/or more meaningful than other community ecology approaches. The aim of this study is to use trait-based approach to assess the relationship between bryophyte species functional diversity and community assembly. We evaluate how bryophyte species functionally interact with their abiotic and biotic environments and how habitat filtering and niche differentiation influence bryophyte assemblages along an elevational gradient. This study was carried out in Marojejy National Park, northern Madagascar. Epiphytic liverworts were collected along an elevational gradient, at 200 m intervals from 250 m to 2050 m (BRYOLAT methodology). Twelve morphological traits potentially related to resource use, life history, species defence, resistance to desiccation and photosynthetic activity are studied. Our results provide evidence that assemblage of epiphytic liverwort community is driven by climatic conditions and vegetation structure, affecting the occurrence of species among and within communities. Liverwort's morphological traits tend to shift from convergent to divergent with an increasing elevation. Higher temperature and taller vegetation appear to have driven a strong functional convergence of size related traits at lower elevations but have allowed for divergence in these at higher elevation. Habitat filtering and niche differentiation along the same transect both explained observed species abundance in communities. Whilst habitat filtering is associated with trait convergence and is strongest at lower elevations, niche differentiation associated with trait divergence occurs at higher elevations and is higher at the most species-rich sites. Other physiological traits related to features such as, photosynthetic capacity and carbon fixation need to be considered in the future to better understand relationships between species composition and ecosystem processes. Environmental filtering and niche differentiation jointly determine species occurrence and distribution within communities. Such result in understanding functional traits diversity of bryophyte assemblages is important notably in the evaluation of Malagasy tropical forest ecosystems state as a basis for conservation planning.

Keywords: Liverworts, Madagascar, Marojejy National Park, Morphological traits, Rainforest

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Ecosystem services associated with water: the role of the liverwort *Frullania tamarisci* along an elevation gradient in Terceira Island (Azores) for one year

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Water is essential to life, and vital to all processes related with the metabolic functioning of plants. Bryophytes depended almost exclusively on external water supply due to their simple morphological features and absence of true vascular tissues. Thus, they tend to mimic the environmental conditions of different areas and seasons, being good indicators of ecological processes. Moreover, bryophytes are able to intercept rain and dew (liquid water) and use fog (water vapour), and transport water both externally, by capillary forces, and internally, in different cells (specialized or not). Thus, bryophytes play an important role in water-flow regulation through their unique water holding ability. Notwithstanding this role, almost no data exists on the quantification of the water inputs into the system. In this study we aimed to know how the Field Water Content (FWC) of a common liverwort species (*Frullania tamarisci*) varies along the year, in three native vegetation stands, at different altitudes in Terceira Island, and how do climate variables (temperature, precipitation, relative humidity, vapour pressure deficit) affect its Relative Water Content (RWC) along the four seasons. In order to quantify the species' hydration status at three different elevation native vegetation stands (40 m, 600 m and 900 m), five samples of approximately 20 shoots were monthly collected in the field, kept in waterproof containers, and later that day weighted in the laboratory, to get FWC. The same samples were then fully hydrated, weighted, oven dried and weighted, to get RWC. As expected, FWC increases along the elevation gradient, reaching 9 g/g during at the highest elevation and about half of that value in the lowest location, during the wettest seasons (winter and spring). RWC values show that the plants keep hydrated for the whole year, albeit never reaching their full capacity, with a yearly average of ca. 40%. Understanding how much native bryophytes, acquire, store, and release water into the system contributes to the knowledge of native vegetation resilience in the face of climate change and, especially, potential impacts on the availability and quality of water - a major ecosystem service performed by plants.

Keywords: bryophytes, ecophysiology, ecosystem services, liverworts, water holding ability

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Functional diversity of the flora of the Canary Islands

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Plant traits that determine under which environmental conditions plants can survive and reproduce have gained increasing interest, especially in the face of rapid global change. However, research on functional traits of island floras has been underrepresented so far. This is despite the fact that islands harbour an exceptionally high diversity of endemic plant species which have adapted to an isolated environment. In this study, we measured the functional differences between all endemic and non-endemic spermatophytes of the Canary Islands (n = 2197) in order to identify how environment drives species' distributional patterns. Therefore, we modelled species' occurrences and collected data on functional morphological traits, associated with resource allocation and dispersal ability. Subsequently, we calculated different measures of functional diversity and analysed the resulting patterns across climatically and topographically-determined zones. Overall, we found that endemic plant species were functionally less diverse and had less extreme trait values than non-endemic plant species (Figure 1). Interestingly, we show that there are only few trait combinations that are exclusively associated with endemism and that many trait characteristics are redundant across endemic and non-endemic plant species. Even across environmental zones species occupied similar sets of the functional spectra. However, functional dissimilarity across environmental zones occurred when endemics where removed from the analyses. All in all, our results indicate that most endemic species are not functionally unique and are able to occupy a broad environmental niche. We conclude that the adaptation of plant species to isolated island environments yields species with a similar set of functional traits suitable for the occurrence across diverse environmental conditions.

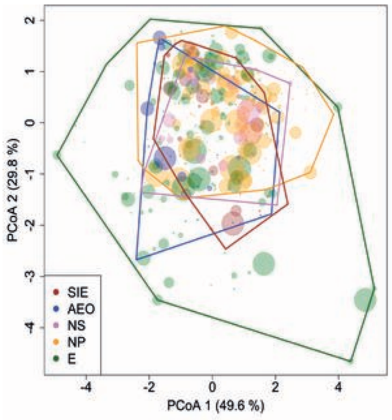

Figure 1 Traitspace of the spermatophytes of the Canary Islands (n = 486 species). Species are plotted within the functional traitspace along PCoA axes 1 and 2 that explain 49.6 % and 29.8 % of the total variation among plant species, respectively. Leaf area was most closely related to PCoA axis 1 (cor = -0.85) and fruit length was most closely related to PCoA axis 2 (cor = -0.79). Circle sizes illustrate the relative occurences of species across all grid cells. Occurences are scaled relative to the most common species. The figure shows the similarity between the functional traitspaces of single island endemics (SIE), archipelago endemics only (AEO), surely natives (NS), possible natives (NP) and exotics (E). Most species were concentrated within a central core region of the traitspace, indicating a high number of morphologically similar species.

Keywords: biogeography, Canary Islands, endemism, functional traits, plant functional diversity

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The importance of accounting for imperfect detection when estimating functional and phylogenetic structure of bird communities on land-bridge islands

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Incorporating imperfect detection when estimating species richness has become commonplace in the past decade. However, the question of how imperfect detection of species affects estimates of functional and phylogenetic community structure remains untested. The goal of this study is to assess how imperfect detection of species biases estimates of different measures of diversity, as well as community structure of island birds. Bird communities were surveyed annually in the breeding season (April–June) from 2007 to 2016 on 36 islands in the Thousand Island Lake, China. We employed multi-species occupancy models to assess the effects of imperfect detection of species on estimates of bird diversity and community structure by incorporating species traits and phylogenies in a land-bridge island system. Our results showed that taxonomic, functional and phylogenetic diversity were all underestimated significantly as a result of species' imperfect detection, with taxonomic diversity showing the greatest bias. The functional and phylogenetic structure calculated from observed communities were both more clustered than those from the detection- corrected communities due to missed distinct species. The discrepancy between observed and estimated diversity differed per the measure of biodiversity employed. Our study demonstrates the importance of accounting for species' imperfect detection in biodiversity studies, especially for functional and phylogenetic community ecology. With datasets that allow for detection-corrected community structure, we can better estimate diversity and infer the underlying mechanisms that structure community assembly, and thus make reliable management decisions for the conservation of biodiversity.

Keywords: Bayesian analysis, detectability, functional trait, habitat fragmentation, phylogenetic diversity

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Landscape structure influences niche-based and neutral mechanisms of community assembly in a fragmented insular dry forest

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Tropical islands often exhibit a singular biodiversity within small areas, making them particularly vulnerable to habitat loss and fragmentation. However, we still lack an integrative understanding of how changes in landscape structure impact the dynamics of these ecosystems. In this study, we address the influence of past and present landscape structure on niche-based (deterministic) and neutral (stochastic) components of tree community dynamics in insular forests undergoing habitat loss and fragmentation. We characterized the current taxonomic and functional (wood and leaf traits) composition of 100 tree communities in a dry forest of New Caledonia that underwent habitat loss and fragmentation over the last decades. We used a mechanistic coalescent-based model to simulate community assembly from the observed species pool under varying parameters of immigration and trait-based environmental filtering. By comparing the composition of simulated and observed communities, we inferred parameter values of environmental filtering and immigration shaping the composition of observed communities (Approximate Bayesian Computation). Then, we used partial regressions to evaluate the relationships between inferred parameter values and landscape metrics (distance to edge, patch area, and habitat amount around communities) derived from either recent or past (65 yrs ago) aerial photographs, while controlling for the effect of soil and topography. We found significant relationships between landscape metrics and both parameters related to environmental filtering and immigration. Environmental filtering was affected by both past and recent landscape structure and were mainly influenced by distance to edge and topography. In contrast, immigration rate was primarily linked to past landscape structure, and was positively correlated to habitat amount surrounding communities. Our results show that landscape structure can influence both niche-based and neutral assembly processes in fragmented landscapes. Recent edges creation can affect environmental filtering, resulting in rapid changes in community composition. Nonetheless, the effects of habitat loss and isolation on neutral migration-drift dynamics may take longer to impact community composition. Recently isolated communities may thus be subject to an extinction debt. Our study highlights the importance to include the history of landscapes into conservation policies to better assess the effects of habitat loss and fragmentation on biodiversity dynamics.

Keywords: landscape, habitat loss, environmental filtering, neutral dynamics, assembly processes

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Resilience of tropical forests to cyclones: an individual-based model simulation approach

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Tropical cyclones can have a major impact on tropical forests, and their intensity is believed to increase in the next decades. In addition, these forests have high level of biodiversity and endemism and are exposed to anthropogenic activities. However, a comprehensive understanding of the long-term effects of tropical cyclones on the structure and dynamics of tropical and subtropical forests has yet to emerge. Here, we coupled an individual-based forest dynamic model, TROLL, with a global climatic boundary condition, the CRU-NCEP re-analysis climate data. We applied this model to a subtropical forest of Taiwan, in a region with the highest frequency of cyclone visits in the world. We showed that the CRU-NCEP data represented reasonably well climatic forcing at the local level. We also compared extreme wind data derived from reanalysis dataset with best-track data (IBTrACS), which specifically track tropical cyclone path and intensity around the world. Baseline simulation results showed adequate fit between simulated and observed forest structure metrics (such as maximum height, tree density, and aboveground biomass.) Wind regimes were related to treefall probability using a bio-mechanic model, accounting for tree allometry, wood density and local neighborhood effect. As the intensity of extreme wind conditions increased, we observed a critical transition from a "forest" state to a "non-forest" state, suggesting a non-linear behavior of the system. A cross-site comparison was performed including sites from the Caribbean region, and showed that the model was also able to capture the dynamics of these forests. Future work should explore the vulnerability of forests to cyclonic events at global scale and under climate change scenarios.

Keywords: climate change, cyclone, forest, tree allometry, treefall

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Conservation

Contents

Who really benefits from the worsening human-wildlife conflict and mass-culling of an endangered island flying fox on Mauritius?

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Island flying foxes (genus Pteropus) are among the most endangered bats worldwide and face many threats including conflict arising over them consuming commercial fruits. Mauritius provided a severe example of such conflict when it mass-culled the last surviving of its three originally present native Pteropus species despite it being already threatened with extinction. The situation provides a rare opportunity to explore possible solutions to a type of threat that is growing worldwide. We surveyed the approaches and arguments used by the principal stakeholders involved both in favor and against mass-culling as the preferred strategy in this human-wildlife conflict and assessed their respective strengths and weaknesses as well as their efficacy in reaching their intended objectives. Although the mass-culling of 2015 and 2016 failed to improve fruit growers profits, government ordered a third mass-cull in 2018 targeting 20% of the already halved population despite the International Union for Conservation of Nature worsening the Red List category of the species from 'Vulnerable' to 'Endangered' a few months earlier. To justify its stance, authorities continue to discard best scientific evidence and reasoning to favor unreasonable claims. The human-wildlife conflict surrounding the flying fox continues to worsen despite appeals and efforts for dialogue from numerous conservation organizations over several years. The lack of intended results from previous mass-culling campaigns did not either bring Mauritius to reconsider its position on ordering mass-culls. Mauritius' stance is consistent with first pitting planters against conservationists followed by taking decisions that superficially appear to support planters. Although this stance does not improve planters' profits, it conveys an impression that boosting profits is government's main concern, and helps rally at least short-term political support in the wake of forthcoming general elections. While conservationists should continue to foster research for innovative solutions and dialogue with politicians as well as education and sensitization of stakeholders to encourage solutions coming from the grass-roots, they should also acknowledge the limitations of these approaches and engage when necessary into more impactful strategies, including litigation. Currently, a case has been lodged in the supreme court of Mauritius against government's decision to mass-cull the Endangered flying fox.

Keywords: conservation, endangered species, fruit bats, Humans wildlife conflict, policy

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Ten years of monitoring and conservation of an endemic island parrot

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The Seychelles archipelago consists of 115 islands and yet the national bird, the Seychelles black parrot *Coracopsis barklyi*, the females of which emit melodious, individually unique calls when breeding, is endemic to only the small (38.5km2) island of Praslin. *Coracopsis barklyi* is the only remaining parrot species in the Seychelles, but with a tiny and highly restricted population, is highly vulnerable to a range of threats including introduced species, habitat change, climate change impacts and disease. Despite its significance, little was known about *C. barklyi* until recently, and it was only declared a distinct species in 2014. Ten years ago a long-term monitoring programme was set up to understand the breeding behaviour, population dynamics and trends, and threats to *C. barklyi.* Methods included nest monitoring, ringing chicks, trapping trials to determine the impact of rats on breeding success, population surveys, mist-netting and ringing adults and disease-screening. Challenges have included *C. barklyi*'s tendency to nest in fragile dead palm trunks that cannot be directly climbed so a new method was developed and is used for nest monitoring. The monitoring programme has overturned previous assumptions; for example that there is a lack of nesting cavities, and that the species breeds on Curieuse. Our monitoring has shown highly variable breeding activity and relatively low overall breeding success. There are sufficient breeding cavities available in most seasons and drivers of low breeding success appear to include invasive species, among other factors. The population appears to be stable but invasive species, including rats and yellow crazy ants, are a significant concern. The presence of introduced ring-necked parakeets *Psittacula krameri* on nearby Mahé island posed a serious threat to *C. barklyi*, due to potential transmission of PBFD virus but the virus has not been detected in *C. barklyi* and *P. krameri* has now been eradicated from Seychelles. This long-term monitoring programme has substantially aided our understanding of *C. barklyi*'s ecology and conservation needs and will inform future conservation actions, such as translocations to other islands. The monitoring programme will continue and should prevent this species from following the Seychelles parakeet, *Psittacula wardi* to extinction.

Keywords: breeding success, invasive alien species, island endemic, long term monitoring programme, parrot conservation.

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*Speaker

Five phases of long-term invasive species management: Lessons from the Amami mongoose eradication project

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In recent years, there is growing evidence that invasive species can be eradicated mainly from small islands, which allows us to recognize eradication as a realistic target for invasive species management. If we can feedback the findings obtained to other projects, we could raise the overall success of invasive species management programs. In this presentation, I introduce an outline of the mongoose eradication project on Amami-Oshima Island (712 km2), Japan, since 2000, which is the biggest mongoose management project. The project has now reached the final phase, where the number of captured mongooses has decreased to only one in 2018, under tremendous management efforts such as by about 2.7 million trap-days, mongoose detection dogs, and pinpoint use of poison bait. Based on the findings of the project, I generalize the roadmap for long term and large island invasive species management by dividing it into five phases. I show that it is necessary that tactics should be updated in the course of the project according to the varying population status. I also show that it is important to establish the governance design, which promotes breakthroughs to proceed to the next phases. In order to establish an appropriate governance, a collaborative system between government, researchers, and residents is needed. Finally, I provided a practical checklist for long term and large island invasive species management. The roadmap and checklist presented in this review are expected to be utilized as guidelines for examining the concept and direction of ongoing various invasive species management programs.

Keywords: recovery of native species, eradication, invasive species management, Amami, Oshima island, governance

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*Speaker

The value of the long-term Seychelles White-eye Recovery programme and challenges faced by the species

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The Seychelles White-eye *Zosterops modestus* is one of the globally threatened endemic species. The White-eye became almost extinct because of the excessive nest predation exerted by introduced rats, particularly the Black rat *Rattus rattus*. As part of the Seychelles White-eye Recovery Programme (SWERP), started in 1998, two successive island translocations were conducted from the original source population on Conception Island to two rat free islands in 2001-03 (Frégate) and 2007 (Ile du Nord). Subsequently, the global population size of this species doubled from c. 300 birds in 1998 to 600 birds in 2012. Consequently, the species was downlisted from Critically Endangered to Endangered in the IUCN Red List. The Seychelles White-eye Species Action Plan requires another two island transfers to bring the species to Vulnerable and eventually down to Near-Threatened status. There are currently no rat-free islands suitable for the species in the Mahé group archipelago. Hence Grande Soeur Island, in the Praslin group which was recently rat-free were considered for a translocation of the White-eye from Conception Island. Moreover, a proposal for the reinforcement of the population on Mahe was considered. During a survey on Conception Island early 2018 it was discovered that the White-eye population had been dramatically reduced from ca. 300 individuals to less than a dozen due to invasion of the once rat-free island by the Black rat. The global population stands at ca. 400 individuals a reduction from 650 individuals in 2014. This stresses the key role of biodiversity and how all these island endemics restricted to islands freed of introduced rats remain highly vulnerable to reinvasion. So the more island populations are retored the better it is for the survival of the species, and this is what is being done as part of the SWERP. The long-term Seychelles White-eye Recovery programme (1998-2019) shows that it is possible to successfully save a species but that there are several challenges that needs to be faced. The success of conservation introductions along island restorations programmes paves the way for other species that faces similar problems.

Keywords: conservation, endangered species, islands, invasions, translocation

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Population dynamics of an endangered endemic seabird of Réunion Island, the Barau's Petrel (*Pterodroma baraui*): implications for conservation

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Island biodiversity is threatened by many factors, such as alien species and habitat destruction. These threats are particularly worrying on islands because a large proportion of island biodiversity consist of endemic species. Réunion Island is the only island in the world where two endemic species of petrels breed, the Mascarene Petrel (Critically endangered) and the Barau's Petrel (Endangered). Both species are threatened by light pollution which attract and disorientate hundreds of fledglings each year and predation by invasive mammals at breeding colonies. Several conservation actions are implemented since several years to reduce both threats: rescue campaigns to save fledglings attracted by lights and cat and rat control at breeding colonies. The goals of our study was to investigate the population dynamics of Barau's Petrel in order to assess the efficiency of these conservation actions. The study was based on 15 years of mark-recapture data and breeding success monitoring implemented at two breeding colonies. Our model suggests that both predator control and rescue campaigns of fledglings attracted by lights, have positive effects on population dynamics. Thus the Barau's Petrel is a conservation dependant species. It's therefore necessary that the conservation actions continue in order to ensure the survival of this species. Our study also shows that coupling population monitoring and conservation actions is crucial to evaluate the efficiency of these actions and to adapt conservation strategies to changes in population dynamics.

Keywords: endemic seabird, conservation, CMR, extinction risk, Indian Ocean

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[*] Speaker

Metabarcoding analysis of endemic lizards' diet for guiding reserve management in the Macaronesian islands

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Islands are considered natural laboratories as they represent simplified models and hold a higher number of endemic and threatened species when compared with the mainland. Therefore, studying their ecological networks is of high importance for developing accurate conservation plans. Interesting study models for evolutionary and ecological studies are the reptiles of the Macaronesian Islands, especially the ones inhabiting remote areas. Some of them present uncommon ecological and evolutionary patterns, and most have simplified trophic webs that remain poorly studied. The diet of the most widespread continental *Tarentola* species is already widely studied using classical methods. However, only one known study was performed using next-generation sequencing (NGS) techniques for this genus and very few for reptiles in general. The main objective was to assess diet composition of two endemic geckos from Macaronesia, the emblematic giant wall gecko of Cabo Verde *Tarentola gigas*, and the Selvagens gecko *Tarentola (boettgeri) bischoffi* of those Portuguese islands, using DNA metabarcoding to provide valuable information to the conservation of these threatened species. Little was known on both their ecology and dietary habits. In the first study, we aimed to compare the diet of the two subspecies of *T. gigas* to discuss options regarding its reintroduction on an island where it went extinct. In the second, we compared morphological and DNA metabarcoding techniques associated to very different sampling efforts to check the impacts on the representation of the Selvagens gecko's diet and discussed advantages and limitations of both methods. Results have revealed that both species are generalists, feeding on plants, invertebrates and even vertebrates. Using metabarcoding, we were able to identify a higher diversity of dietary items, many that formerly went unnoticed, with generally higher taxonomic resolution than using traditional methods, and to reveal that plants have a significant role in their diets. They also revealed the importance of expeditions to remote areas, such as Monaco Explorations, to decrease knowledge gaps. Overall, the information revealed by these ecological networks is important for the development of conservation plans on these protected areas and reinforce the important and commonly neglected role of reptiles on island system.

Keywords: conservation genetics, protected Areas, remote areas

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Endemic plant species are more palatable to introduced herbivores than non-endemics

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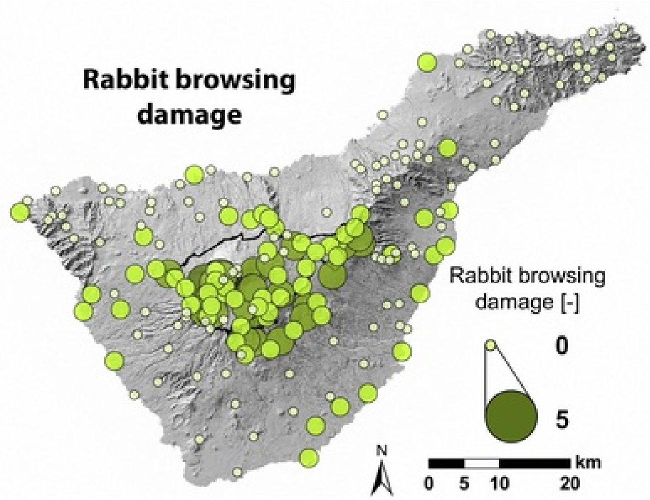

Oceanic islands harbour a spectacular diversity and unique species composition, thus being major contributors to global plant biodiversity. This uniqueness is mainly a result of endemic plant species that have evolved in-situ, often in the absence of mammal herbivores. However, island endemism is under severe threat by introduced herbivores, especially generalist herbivores such as the European rabbit (*Oryctolagus cuniculus*). The European rabbit has been introduced to a large number of islands around the world, where it has been recognized as a major threat to island plant species and island ecosystems. We test the long-standing assumption that endemic species are particularly vulnerable to generalist introduced herbivores (European rabbit) using an unprecedented dataset covering an entire island (n = 210) with enormous topographic, climatic and biological diversity (Tenerife, Canary Islands). We find that, with increasing endemism, plant species are more heavily browsed by rabbits than non-endemic species with up to 67% of endemics being negatively impacted by browsing. This indicates a dramatic lack of adaptation to mammal herbivory in endemics, making endemics much more palatable to introduced generalist herbivores than native non-endemic or non-native plant species. Further, ecosystems with a high percent endemism are most heavily browsed, suggesting ecosystems-specific vulnerability to introduced herbivores, even within islands. Interestingly, rabbit density is a poor predictor of browsing damage, illustrating that ecosystems-specific density-damage relationships exist. Thus, conservation initiative should consider applying ecosystem-specific rabbit densities as basis for management efforts. To protect global biodiversity offered by disproportionally high endemism on oceanic islands ecosystem-specific herbivore control and eradication measures are of highest priority.

Keywords: Conservation, island endemism, invasive species, mammalian herbivory, European rabbit

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Great genetic diversity but high selfing rates and short-distance gene flow characterize populations of a tree (Foetidia; Lecythidaceae) in the fragmented tropical dry forest of the Mascarene islands

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Following the global trend of deforestation and degradation, tropical dry forests in the Mascarenes archipelago on Reunion has undergone harsh reduction and fragmentation within 3 centuries of human occupation. We investigated the genetic diversity, mating system, and gene flow in fragmented populations of the native tree *Foetidia mauritiana* (Lecythidaceae) on Reunion, using microsatellite genotyping of adults (in- and ex situ) and seed progenies (in situ only). To test genetic isolation between the Mascarene islands, we also genotyped conspecific adults on Mauritius, and trees of *Foetidia rodriguesiana* on Rodrigues. We found a high genetic diversity among the trees on Reunion, but no population structure (G'ST: 0.039–0.090), and an increase of the fixation index (FIS) from adults to progenies. A subsequent analysis of mating systems from progeny arrays revealed selfing rates $> 50\%$ in fragmented populations and close to 100% in lone trees. A paternity analysis revealed pollen flow ranging from 15.6 to 296.1 m within fragments. At broader scale, the populations of *F. mauritiana* on Reunion and Mauritius are genetically differentiated. The morphologically allied taxa *F. rodriguesiana* and *F. mauritiana* are clearly isolated. Therefore, this case study shows that genetic diversity may persist after deforestation, especially in long-lived tree species, but the reproductive features may be deeply altered during this process. This would explain the low seed production and the absence of recruitment in *F. mauritiana*. Restoration programs should take into account these features, as well as the importance that trees ex situ represent in restoring and conserving diversity.

Keywords: genetic erosion, habitat fragmentation, island biota, mating systems, pollen dispersal, tropical dry forests

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Are humans decreasing species diversity or only phylogenetic diversity in mammals on islands?

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837 out of the 5750 non-marine mammalian species that have existed within the last 130,000 years are (or were) endemic to isolated islands. Due to human actions 127 of the island endemic species, along with 225 other species are sadly now extinct. Based on their IUCN categories we can expect that another 202 island endemics and 461 other species are expected to go extinct in the next 100 years under a status quo model. The total diversity of island endemic mammals in 100 years may thus only be 61% of the species that could have been. The question is however if we also could at the same time have increased speciation rates. I.e. if we in 100 years manage to reduce extinction rates to background levels, would the geological consequences of humans be a reduction in diversity or rather an increase in species turnover? To understand this we mined the literature to get full lists of all introduced mammals to both continents and to isolated large and environmentally stable islands. We found a total of 68 such introductions to continents and 1129 to 173 islands, altogether representing 130 currently accepted species from 13 different orders. Some islands may be too small to contain stable populations of some of the species, but an estimated 925 island introductions have been to islands which plausible can maintain viable populations (estimated carrying capacity $>$ 500 individuals). These introductions are not currently given species rank, but represents isolated populations without current gene flow and without any plausible potential for future non-human-mediated gene flow. If we were to treat these as species, which they all else equal likely will develop into, our results therefore suggest that humans may not decrease species diversity globally and in particular not on isolated islands. Considering phylogenetic diversity, in contrast simulations show that human extinctions have dramatically reduced global phylogenetic and that this reduction likely will take millions of years to recover. I.e. over geological time, the persistent signal of humans may be a reduced phylogenetic diversity and an increased species turnover, but not a reduced (mammalian) species diversity.

Keywords: mammals, introduced species, extinctions, phylogenetic diversity

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*Speaker

Systematic conservation planning in New Caledonia: supporting sustainable land-use policies with reserve selection models

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Habitat degradation, fragmentation, and destruction are today the leading causes of species extinction on Earth. A major challenge for environmental managers, hence, is to efficiently balance land use between economic development and conservation of natural habitats. In New Caledonia, the smallest biodiversity hotspot in the world, finding this trade-off is tedious. In particular, the conservation of its highly diverse forest ecosystems, distinguished by high rates of endemism, can be conflicting with mining activity, the major economic sector of New Caledonia. Managers are willing to study how to refine decisional processes through the use of systematic conservation planning and computational sustainability. To this end, we considered the project "Côte Oubliée" started in 2016 by the environmental managers of the South Province of New Caledonia. It aims at delineating a complex reserve system (including about 1200 km^2 of terrestrial and 950 km^2 of marine reserve) in the southeast of New Caledonia in an area with rich biodiversity and overlapping with different socioeconomic interests (such as 238 mining concessions, private and cultural lands, and fisheries) as well as 135 km^2 of area to be restored. Our objective was to identify how the reserve could be efficiently delineated while respecting socioeconomic constraints. More precisely, we focused on the biodiversity representation as much as on the spatial configuration of the reserve. Additionally, we aimed at reducing fragmentation through the identification of areas suitable for ecological restoration. Relying on a constraint-based reserve selection model, we iteratively considered operational scenarios and produced maps providing the basis for decision support. The model was then refined according to a feedback loop between managers and scientists. Through this iterative process, we could suggest a delineation of the reserve that maximized the representation of biodiversity features while satisfying managers constraints. We also highlighted key areas for reducing fragmentation through ecological restoration. This real-world pilot study showed how systematic conservation planning can provide the basis of a decision support framework for conservation, through reserve selection models. Beyond that, it showed how the iterative use of such a framework could help to reduce the gap that can sometimes exist between scientists and managers.

Keywords: New Caledonia, systematic conservation planning, computational sustainability, reserve selection

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A science and conservation success story: insights from 30 years of research on Seychelles warblers

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Once brought to the brink of extinction due to habitat destruction, the Seychelles warbler population has made a spectacular recovery following intensive conservation efforts. These conservation efforts were so successful that this species is no longer threatened with extinction. Apart from being a prime example of successful conservation, the Seychelles warbler has also become an iconic model species for ecological and evolutionary research. It has been studied intensively since 1985 and this long-term research program has yielded numerous significant insights in conservation, ecology and evolution. Intriguingly, this species went through a many-year bottleneck of only 25 individuals, but it does not seem to have suffered from the resultant high degree of inbreeding. We showcase how targeted conservation efforts, including habitat restoration and translocations, have saved this species from extinction and highlight the importance of long-term monitoring programs and in-depth knowledge of the species' ecological requirements, life-history and previous conservation actions. In addition, we show several scientific highlights of the ongoing long-term study, including new insights into the evolution of sociality and ageing and the impacts of inbreeding and genetic variation on behaviour. Our results show how scientific research and successful conservation go hand in hand and underline the crucial importance of long-term studies for successful conservation of island species and ecosystems.

Keywords: Seychelles warbler, Birds, Translocations, Inbreeding, Cooperative Breeding, Ageing, Long term studies

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*Speaker

Biodiversity conservation needs on European overseas islands: lessons from Macaronesia

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In the middle of the double crisis of global warming and mass extinctions, the effectiveness of measures to conserve Earth's biodiversity must be permanently assessed. This is particularly true on islands, given their known features of high endemism and ecological frailty. With about 5,300 terrestrial and nearly 400 marine endemic species, the Atlantic islands of Macaronesia are an ideal place to focus conservation efforts- and to check the effectiveness of existing ones. In the framework of the BEST Initiative, we compiled information on the distribution of threatened species in the Azores, Madeira and the Canaries, using IUCN's Red List criteria. With this geographic information we proposed Key Biodiversity Areas (KBA) and compared them with the existing network of protected areas, including Natura 2000. Our list of threatened species totaled 656, most of them plants and molluscs. The Canaries hosted more than half of these species, reflecting its higher endemism density. Almost all species (90%) are endemic to Macaronesia, often to a particular island, and nearly one third are critically endangered. There was a knowledge bias against smaller, less mobile, species, like insects. The number of threatened species is therefore underestimated. A lack of data on the geographic distribution was also noted, affecting e.g. two thirds of the fish species and 40% of the reptiles. Even so we proposed 194 KBAs (of which 46 designated as priority because they represented the only known site of at least one endangered species) covering nearly a quarter of the land area. Surprisingly, after decades of conservation efforts, we found that 16 of the priority KBAs are only partially enclosed in protected areas, while 8 enjoy no protection whatsoever. Our study revealed important gaps in the knowledge of Macaronesian biodiversity and of its conservation status. It also showed the insufficiency of existing legislation and practices, from the regional level up to the European Directives, which do not list as prioritary many globally threatened species. If the objective of stopping biodiversity loss in Europe is to be reached, investments in basic science and monitoring must increase, and conservation actions must follow the resulting knowledge.

Keywords: Natura 2000, endangered species, protected areas, key biodiversity areas

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Evidences of global warming on island coastal biota: lessons from the Azores

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Global warming is having a profound effect on every world ecosystem. The intertidal and shallow subtidal habitats of small oceanic islands are particularly vulnerable, given their restricted area, smaller population size, isolation and exposure to climatic elements and human activities. In the present work we review the main results of our work on the coastal ecology of the Azorean communities. Characterization studies were coupled with experimental work to shed light on the challenges facing the conservation of the coastal biota and to point out strategies to deal with it. Rising seawater temperature and changes in oceanic current patterns are known to be responsible for the arrival of new species and the disappearance of others. Recently introduced or already established non-native species in the Azores (like algae from the genus *Caulerpa* and *Asparagopsis*) have potential or ascertained impact on the native coastal communities. Moreover, changes to the relative abundance of species have also been observed: the increased abundance of herbivorous fishes, for instance, is having an effect on keystone algae species, which is compounded by unsustainable algae exploitation practices. Finally, sea level rise and the increasing frequency and magnitude of extreme events is leading to the artificialization of significant areas of coastline, with the construction of an increasing number of breakwaters, jetties and other human-made structures. In the Azores this has caused habitat loss and fragmentation, resulting in decreased abundance and diversity of intertidal biota, with the consequent decline of ecosystem services. The research reviewed in this presentation has had some impact on local regulations, e.g. on setting up marine reserves or fisheries management plans. This highlights the importance of maintaining local scientific expertise in support of the decision-making process in small oceanic islands to face the scale and speed of the predicted changes in the oceans.

Keywords: global warming, coastal urbanization, overexploitation, keystone species, community structure

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A model-based evaluation of reefs connectivity and habitat degradation scenarios - Implications for future marine spatial planning and marine conservation policies in the Western Indian Ocean

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Coastal and marine ecosystems are under increasing pressure from a wide variety of threats such as habitat degradation, overfishing, offshore energy development, and climate change. As marine ecosystems degrade, so do the well-being and livelihoods of populations that depend directly on the ecosystem goods and services they provide. Marine protected areas have been proposed to protect biodiversity, restore damaged ecosystems, sustain fisheries, and rebuild overexploited stocks. The effectiveness of MPAs depends in part on their effectiveness as connected networks, linked over large areas by ecological processes such as larval dispersal. The CBD AICHI Target 11 calls for 10% of coastal and marine areas to be conserved by 2020 through effectively managed, ecologically representative and well connected systems of protected areas, and integrated into the wider landscapes and seascapes. According to the Regional State of the Coast Report (UNEP-Nairobi Convention and WIOMSA, 2015), "there is need for immediate and substantive actions to increase the adaptive capacity of coastal marine ecosystems and the people that depend on them, especially in relation to MPAs". In order to better assess the situation in the Western Indian Ocean, we applied a biophysical model driven by ocean currents to evaluate connectivity between reefs. We applied graph-theoretic analysis, including clustering and a betweenness centrality metric. Our results show high interconnectivity within several sub-regions and lower connectivity across the WIO region. We compared the results with the current MPA network, and proposed sites/reefs that should be considered priority sites for MPA implementation: Pebane, Cosmoledo, Majunga, Masoarivo, Platte Island, Farquhar, Agalega and Geyser bank. The next step of this work is the generation of scenarios to study habitat degradation consequences on coral reef ecosystems connectivity patterns in order to better support decision-making. Results are discussed in terms of implications for transboundary marine policies and regional cooperation in the WIO. This work was conducted within the framework of the SIREME (IRD) and MASPAWIO (IUCN) projects.

Keywords: Coral reefs, connectivity, conservation, marine protected area, fishery management, larval duration, remote sensing

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Individual variation in invasive island predators: consequences and management implications

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Individual variation has been identified within a broad range of taxa as key to understanding ecological, evolutionary and conservation outcomes, but there remains limited information on such variation among invasive individuals. Invasive species remain one of the most critical threats to a wide range of island biota and communities, and such differences among individuals can have important consequences for determining variation in the impacts and fitness of invaders in novel environments. In addition, understanding such impacts would provide important insights to guide management actions. Using a natural experiment across islands invaded by different species assemblages within the Hauraki Gulf, NZ, we determined the extent and covariance of individual variation across dietary and behavioural traits in two invasive rat species in the wild. This allowed us to explicitly test how both competition (between rat species) and predation (by invasive cats when present) modulate invasive individuals' behavior and ecology. In addition, this enables the identification of trait combinations, i.e. individual phenotypes, that result in individuals disproportionately affecting native biota. We found substantial behavioural differences among individual rats both within and between species; and within and between island locations. However, relationships between behavior and diet were complex and varied between locations, potentially mediated by density-dependent effects. These results have important implications for the theoretical understanding of the individual niche, and for applied management. They highlight how conservation actions may be triaged, particularly in situations where eradication is not currently feasible, to ensure maximum effectiveness through adapting control strategies to target those individuals that pose the greatest potential risk.

Keywords: behaviour, diet, individual variation, invasive species, niche, stable isotope analysis

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Impacts of climate change on invasive plants in small islands: the case of Azores

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Biological invasions are a recognized serious problem for small islands. The effect that climate change can have on these invasions is still uncertain. It is commonly believed that the predicted raise in temperature and altered precipitation will favor the establishment of invasive alien species (IAS). For the case of plants, many studies have ascertained how IAS will be distributed in the future. However, these distribution predictions change greatly from location to location, with different findings depending on the hemisphere. It is thus imperative to study how the established invasive species' distribution will change with the predicted climate change, especially for islands. Islands are hotspots of biodiversity and the spread of invasive species can become a serious problem for native ecosystems. This study aimed to ascertain how the predicted climate change will affect the potential distribution of some of the main invasive plant species present in the Azorean archipelago. For this we deliberately chose the "worst case scenario" RCP8.5 for the climatic data as a precaution strategy based on the historical and still actual trend on the greenhouse emissions. We then used the off-the-shelf BIOENSEMBLES software, to model the species distributions for two time periods, 1969-1990 and 2080-2099, and for the two main islands of the Azores, São Miguel and Terceira. We found that for most cases the potential distribution of the species decreases (21 of the 24 studied species). Only three species showed an increase of the potential distribution on both islands (*Acacia melanoxylon*, *Persicaria capitata*, *Ricinus communis*). These species are projected to increase their distribution towards inland on both islands, where most of the native natural vegetation is located. These species are very serious invasives, which are difficult to control, and can cause serious loss of natural biodiversity. Using the information from these projections can be very useful for decision makers when deciding the managing strategies towards invasive species in the future.

Keywords: invasive plants, climate change, species distribution models, conservation strategies, Azores

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Ecology on Islands

Contents

What is biodiversity? How to better observe it and understand it in the 21st century?

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Until the end of the 19th century, biodiversity data collection was focusing on species taxonomy, collecting specimens with few field notes often limited to the country of origin. As floras became more refined, biologists started to dedicate more effort to the data related to their species observations, adding notes on the exact locality and finally exact coordinates when GPS became available, just a few decades ago.

Nowadays, recording accurately georeferenced species observations has become the norm which, combined with gazetteers of georeferenced localities, allows to generate detailed species distribution maps essential for biodiversity studies. But biodiversity is more than being about species and where we find them. Recording accurate information on the habitat and on population state is still widely considered as optional metadata to species records (as was the exact locality for the 19th century botanist). As a result, species distribution maps contribute very little to knowledge on ecosystem distribution, very little on the species ecology, and very little on the stage of species invasion for different types of habitats of different regions.

Here we present an information system, developed in Seychelles but applicable worldwide, which is based on observation and databasing of biodiversity using four reference indexes: taxonomic, geographic (TDWG), ecosystemic and populational. The ecology of sites where biological observations are made is characterised by the detailed observation of 'ecosystem characters' (substrate, drainage, etc.) using standardized terminologies that are made available to the observer directly on the field through a smartphone-based data collection system designed with Open Foris Collect Mobile. We believe that such a system is the key to enabling the collection of virtual ecosystemic specimens leading to progress in ecosystem taxonomy. The data collection system is compatible with most of the habitat classification systems developed during the last few decades, by combining hierarchy and modularity, and by combining relative scales. We believe that a more complex vision of biodiversity focused on direct observations on the field will be essential to better understand biodiversity at species and ecosystem levels.

Keywords: ecosystemology, biodiversity, smartphone, field inventories, data collection

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Decreasing dominance of the endemic tree *Uapaca bojeri* drives the spread of Pinus in the sclerophyll Tapia forest, Madagascar

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The sclerophyll Tapia forest, which is dominated by the endemic tree *Uapaca bojeri* (Phyllanthaceae), is the last remaining highland forest of Madagascar. The Tapia forest contributes food, wood fuel, medicine and more than 7% of the local population income. However, the forest is threatened by the spread of *Pinus spp* (primarily P. kesiya), which were introduced as a timber source. Well known as a soil acidifier, pine causes the exclusion of several species. The aim of this study was to determine which factors influence the spread of *Pinus* in the Tapia forest. This was achieved by observing the natural spread of pine in the area of Arivonimamo II. One hundred and twenty-five transects, each containing 3 plots of 100m2, were inventoried. In each plot, an inventory was done and environmental (biophysical and topographic) conditions were recorded. Generalized linear models were used to identify the explanatory variables linked to the spread of *Pinus* and to create an appropriate modeling framework. The results showed that the presence and abundance of *Pinus* is highly influenced by the importance value of *U. bojeri*, then by the propagule pressure. The invasion rate of *Pinus* increased i) as the dominance of *U. bojeri* decreased and ii) as the distance between the *Pinus* source and the nearest forest fragment decreased. Other factors, such as high cover of the herbaceous layer and slope, also contributed moderately as explanatory variables. Thus, the model obtained demonstrates the importance of considering the dominance of *U. bojeri* and the location of the pine source for improving predictions of pine invasions. However, invasive pines present a special challenge for management, as they are locally important forestry trees. To manage this landscape efficiently, the Tapia forest needs to be reforested with *U. bojeri* and the pine source should be removed when close to the forest.

Keywords: Exotic tree invasion, Pinus sp., Sclerophyll Tapia forest, Madagascar.

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Lone fighters or team players? How co-occurrence patterns shape the patchy vegetation in arid volcanic environments

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Patchy vegetation is characteristic for harsh environments such as arid and semi-arid areas. Biotic interactions are suggested as one of the main drivers of patchiness in vegetation. The role of positive interactions between species (often referred to as *facilitation*) is even expected to increase with harshness and might thus have apparent impact on species composition of vegetation patches with harshness. However, differentiating facilitative interactions from further underlying mechanisms, e.g. microtopographic heterogeneity, is a non-trivial task. In this study we analyzed the co-occurrence relationships of vascular plant species that form a patchy vegetation in arid lapilli fields (tephra) from recent volcanic eruptions on La Palma, Canary Islands. Assuming a harshness gradient negatively correlated with elevation because aridity is high at low elevations, we expected pronounced co-occurrence (indicating positive biotic interactions) within patches close to the coast in contrast to more benign sites at higher elevations. Our study area offers the unique opportunity to analyze biotic interactions that lead to the formation of patchy vegetation, as lapilli soils are found at all selected sampling sites. We analyzed a total of 1280 shrubby vegetation patches in terms of species composition at 64 different elevational sampling points, ranging from the coast to around 700 m a.s.l. Further parameters regarding the shape, the biotic and the microtopographic neighborhood of the patches were recorded to consider their potential impact on the patch establishment, respectively. A co-occurrence analysis revealed that half of the analyzed species pairs relationships are distributed non-randomly. We furthermore even found three species which matched our strict requirements for a potential facilitator species and that likely enable the establishment of other species within individual patches. Subsequent linear models were used to analyze those patterns along an elevational gradient representing our assumed harshness gradient. Despite our expectations, we did not find the presumed harshness gradient towards coastal sites. This might rather highlight the homogeneity of the environmental conditions on dry lapilli fields on La Palma, even over long distances, than reject the predictions of the stress-gradient hypothesis.

Keywords: facilitation, Oceanic Island, plant plant interactions, stress gradient hypothesis, volcanic substrate

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Grassland habitat islands in urban areas: testing ecological theories

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During the past millennia urbanization considerably changed natural ecosystems and formed new artificial habitat islands. Habitat loss and changes in the abiotic environment are seriously affecting urban biodiversity. We investigated the effect of urbanisation on the grassland vegetation islands in the city of Debrecen, East-Hungary (Europe). Along an urbanisation gradient we studied three kinds of habitat islands (vacant lots, urban parks, and peri-urban grasslands) with five spatial replicates of each habitat type, and five random plots in every site. We tested the following hypotheses: (i) species numbers increase with increasing island area in fragmented urban landscapes, as predicted by the theory of island biogeography; (ii) according to the increasing disturbance hypothesis lower species numbers and diversity, and higher ratio of weeds and disturbance-tolerant species is present in the city centre, (iii) the ratio of warm- and nitrogen-demanding species increases towards the city centre, (iv) we also tested if there is an increase in cosmopolitan and alien species and a decrease in species of the natural flora towards the city centre as predicted by the urban homogenization hypothesis. We found a positive species-area relationship for the permanent habitat islands, while such relationship was not detected for vacant lots. The most intensively disturbed urban parks harboured the lowest number of species and the lowest Shannon diversity. The ratio of weeds and disturbance-tolerants was the highest in the city centre (vacant lots and urban parks) likely due to the high-intensity trampling and soil disturbances. Plant species of the city centre were more drought-tolerant compared to peri-urban grasslands. The ratio of nitrogen-demanding species was the lowest in the urban parks, and the highest in the peri-urban grasslands due to the high nitrogen deposit in the cities. We found that the ratio of alien species were high both in vacant lots and peri-urban grasslands. Ratio of cosmopolitan species was significantly higher in urban parks compared to vacant lots and peri-urban grasslands. Our results suggest that urban habitats have some biodiversity conservation potential. But classical ecological theories may fail in urban environment. This is not just 'new' environment, but new prospect for ecological theories.

Keywords: urbanisation, gradient, urban homogenisation hypothesis, cosmopolitan, increasing disturbance hypothesis

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Diversity of grassland habitat islands: habitat and landscape filters of plant establishment in agricultural landscapes

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Landscape and habitat filters are major drivers of biodiversity on small terrestrial habitat islands by influencing species dispersal and extinction events. In our study we aimed to assess the effects of landscape and habitat filters on the species richness, abundance and trait composition of grassland specialist and generalist plants in small grassland islands embedded in agricultural landscapes. We studied traits related to functional spatial connectivity (dispersal ability by wind and animals) and temporal connectivity (clonality and seed bank persistence). We sampled herbaceous plants, landscape (local and regional isolation) and habitat filters (inclination, woody encroachment and disturbance) in 82 grassland islands in Hungary. The studied grassland islands were preserved by ancient burial mounds, which being sacred natural sites of the steppe region, can provide refuge for grassland habitats even in intensively used landscapes. We used model selection (Akaike's Information Criterion) and fitted GLMs for all possible combinations of the studied explanatory variables to assess the effect of the landscape and habitat filters on the species richness and the percentage cover of the studied functional groups. We found that isolation decreased the abundance of good disperser specialist plants due to the lack of directional vectors transferring seeds between suitable habitat patches. Clonality was proven to be an effective strategy, but persistent seed bank did not support the survival of specialist plants in isolated habitats. Generalist plants were unaffected by landscape filters due to their wide habitat breadth and high propagule availability. Clonal specialist plants could cope well with the increasing woody encroachment due to their high resistance against environmental changes; however, they could not cope with intensive disturbance. Steep slopes providing environmental heterogeneity had an overall positive effect on species richness. Specialist plants were influenced by the interplay of landscape filters influencing their abundance and habitat filters affecting species richness. Landscape filtering by isolation influenced the abundance of specialist plants by regulating seed dispersal. Habitat filters sorted species that could establish and persist at a site by influencing microsite availability and quality.

Keywords: biotic interactions, dispersal filter, landscape composition, spatial connectivity, temporal connectivity

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Evolution on Islands

Contents

Genetic structure of two genera of Sumatran frogs trace back to ancient volcanic islands origins rather than paleodrainage systems

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The influence of riverscapes on the distribution and genetic structure of species has been investigated in various taxa and regions. In most cases, the influence of river systems on genetic diversity depends on taxa specific life history traits as well as other geographic factors. Here, we assess the role of the paleodrainage systems of the Sunda region (with a focus on the island of Sumatra) in shaping the evolutionary history frogs' genera (*Huia* and *Sumaterana*) that are highly dependent on cascading stream habitats during their larval stage. Our phylogenetic analyses demonstrated that paleodrainages had no congruency with the current distribution patterns of *Huia* and *Sumaterana*. Our time divergence analyses estimated these frogs to have colonized Sumatra much earlier than the occurrence of the known drainage systems in the Pleistocene. Interestingly, both genera are genetically structured into northern and southern lineages on the island of Sumatra, which may suggest that the genetic segregation observed today dates back to now connected Sumatran precursor volcanic islands. Our data further corroborate the current underestimation of biodiversity on Sumatra and show that frogs of the genus *Huia* in Sumatra and Java are more diverse than currently known.

Keywords: Amphibians, diversification, gastromyzophorous tadpoles, molecular phylogenetic, Pleistocene, Ranidae, Sundaland

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Factors of population divergence and past demographic history in an endemic tree (*Coffea mauritiana*) from Reunion Island

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Oceanic islands provide unique systems to uncover ecological and evolutionary processes in species. Geographic isolation in combination with habitat diversity have favored processes of speciation and population divergences, leading to high rates of endemism and patterns of local adaptation. However, isolation also resulted in higher vulnerability to external disturbances, such as global climatic changes. Displaying large environmental gradients at small spatial scale, the recently emerged Reunion Island (about 2 Ma), appears as an exceptional laboratory to support such evolutionary studies. *Coffea mauritiana* is an endemic tree species from Reunion Island and Mauritius. Using genetic approaches, this study aimed to: (1) investigate population divergences of a widespread woody species in Reunion Island; (2) assess the impact of past climatic events on the species demography and its potential ecological niche. A large sampling of *C. mauritiana* was performed in Reunion Island, followed by genotyping-by-sequencing. Genetic diversity analyses revealed that *C. mauritiana* populations clustered in regional groups. The low dispersal abilities of the species and the heterogeneous rainfall pattern were pointed out as the main factors contributing to population divergences. Furthermore, SNP markers from a representative set of the *C. mauritiana* species were used to explore the past demographic history of the species. Demographic inferences revealed a reduction in the effective population size of *C. mauritiana* during the Last Glaciation Maximum (LGM). By comparing scenarios of paleo-distribution of the species with the present genetic diversity data of the species, a loss of habitat in the western part of the island was suggested in association with a decrease in rainfall and temperature. In conclusion, results on the distribution of *C. mauritiana* genetic diversity provide guidance for the management of plant conservation on the island. The present work also emphasizes the importance of heterogeneous rainfall pattern as a factor of population differentiation in Reunion Island. Finally, studying the past history of the species provides new insights into Reunion Island forest response to climate change.

Keywords: population divergence, Reunion island, paleoclimate, demographic history, ecological niche modeling

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Niches in time: Molecular gut content analysis reveals changing ecological relationships among Hawaiian Tetragnatha spiders along a chronosequence

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Understanding the ecological dynamics of adaptive radiation is a key step toward identifying the nature and timing of the evolutionary processes behind such striking systems. The adaptive radiation of Hawaiian *Tetragnatha* spiders presents an ideal study system for exploring these dynamics: with *ca.* 50 species displaying a wide range of morphological and ecological traits, many of these species co-occurring with one another, this group offers an exceptional opportunity to explore niche ecology in an evolutionary context. Moreover, Hawaii's geologic age structure, from oldest in the northwest to youngest in the southeast, enables inferences on past processes based on present-day patterns in younger habitats. We characterize trophic niche dynamics within the Hawaiian *Tetragnatha* radiation along a temporal gradient (chronosequence) across the islands of Hawaii, Maui and Oahu. Using molecular gut content metabarcoding, we identify the diets of 23 different species belonging to two clades, which correspond to fundamentally different hunting strategies: web building versus active hunting. We measure the extent to which dietary repertoires overlap on each of the islands, thereby testing how trophic niche dynamics change along the chronosequence. Based on taxonomic classifications of prey to both order and operational taxonomic unit (OTU) levels, we uncover a complex pattern of dietary niche relationships among *Tetragnatha* species over time. As expected, the two hunting strategies are associated with significantly different diets, a pattern which is especially apparent at the ordinal level of prey. Notably, we also find an apparent decrease in dietary overlap as island age increases, suggesting that the degree of dietary niche partitioning may increase with evolutionary time in this group. Our results largely match expectations based on theory, which predicts that species in younger communities should exhibit high niche overlap while those in older communities show pronounced niche differences.

Keywords: trophic niche ecology, adaptive radiation, Hawaii, chronosequence, metabarcoding, next generation sequencing, gut content analysis

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*Speaker

The genomics of founder events in an island colonising bird

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The role of founder events in shaping the evolutionary trajectory of newly established populations has been a topic of sustained interest in evolutionary ecology. A main focus has been understanding how genetic drift during population founding, and in subsequent generations when population sizes remain small, affects genetic diversity and ultimately evolutionary potential. Both theory and empirical data show that in general, strong and long genetic bottlenecks are required for radical losses of diversity. However, the stochastic loss of some alleles, and shifts in relative frequencies of alleles have the potential to limit and promote responses to selection in novel environments. Genomic methods have provided us with the ability to examine both neutral and selected alleles during colonisation processes. We examine genomic variation in a well-characterised system of naturally-colonised and human-introduced island populations of a bird, the silvereye (*Zosterops lateralis*), in the southwest Pacific. Using RADseq data, we assess the genomic impact of founding events on genetic diversity and follow the fate of loci under selection, across a series of historically documented, sequential island colonisation events. We found stronger evidence for loss of diversity in populations seeded from human introductions compared to natural colonisations. Despite the sequential nature of colonisation, and repeated phenotypic trends of increased body size in insular silvereyes, loci under selection were idiosyncratic across populations, likely reflecting the polygenic nature of the repeated phenotypic response to island dwelling.

Keywords: genetics, selection, bird, south Pacific, microevolution

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Chloroplast haplotype analysis of Canary islands Micromeria indicate inter-island colonization as factor to explain genetic diversity patterns

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Genetic diversity on islands in archipelagos might be significantly shaped by interisland geneflow. While this might on one hand contribute to increased diversity levels within islands it also might homogenize differences between islands in species or species groups if hybridization exist. This might lead to the impression of a monophyletic origin of island taxa and to an underestimation of evolutionary distances between species, especially if sequence data from organelles are studied. Here we investigate chloroplast haplotype diversity for Micromeria of the Canary islands. A recent morphological revision and molecular data support that the genus consist here exclusively of single island endemic species. Phylogenetic and nuclear genotype analysis show that geneflow between the species exist and evolution of the genus is highly influenced by hybridization. We constructed a network of chloroplast haplotypes using multilocus Next Generation Sequencing approaches to increase resolution compared to earlier studies. Around 500 samples were investigated for the archipelago comprising all species and islands which are assigned to 94 haplotypes defined using 5500 bp of 11 loci. All marker systems investigated so far, show very strong connectivity between the younger islands of the archipelago. CpDNA shows low genetic structure between some of the islands that result from the pattern of shared haplotypes. Species can have multiple haplotypes in common also between islands which strongly indicate sequential interisland colonization as seeds, especially between La Gomera, Tenerife, and La Palma. The pattern suggest, that when single colonizers arrive as seed, they might hybridize with already established individuals as pollen donors. Because chloroplast DNA is inherited maternally, resulting populations contain then the haplotypes of the colonizer. Such a model would explain inconsistencies between cpDNA and nuclear markers: Within islands different haplotypes can be found in species with low nuclear genetic diversity, between islands haplotypes can be shared in different species with high nuclear genetic diversity. The model would also explain the persistence of the different cpDNA markers in the species even if probably originated from single colonizing individuals. Overall, this can lead to high diversity of cpDNA markers within an island.

Keywords: cpDNA haplotypes, NGS, interisland, colonization, genetic diversity, Micromeria, Canary islands

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Adaptive consequences of introgression during the differentiation of Micromeria in the Canary islands

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Introgression can contribute to the transfer of adaptive traits from allowing for species to occupy new ecological conditions. This process will be more prominent in species that underwent continuous gene-flow during the differentiation process, which is the case of the *Micromeria* endemics form the Canary Islands. This genus has a group of six species sharing morphological traits but with different origins indicating convergent evolution, however without an apparent ecological significance. Previous studies shown that hybridization, promoted by continuous inter island colonization, shaped the distribution of genetic diversity for these endemics. The resulting introgression amongst could also have contributed to the distribution of similar traits in different lineages having some of these adaptive potential. We tested this hypothesis by evaluating the phylogenomic relationships of *Micromeria* and potential introgression patterns, with special focus on these six species. Phylogenies were calculated using coalescent and non-coalescent approaches to evaluate the impacts of incongruent phylogenetic signal. Evidences of introgression were search based on D-statistics. Although with coalescent methods the phylogenetic pattern was congruent with species delimitations, this was not the case when a concatenated matrix was analyzed being rather related with ecological conditions for some of the populations. This was the case of the *M. canariensis* populations restricted to the laurel forest in Gran Canaria that are closer related with *M. gomerensis* from La Gomera than to the other conspecific populations. Introgression involving these species was also found, which may be behind the incongruence topologies found between coalescent and non-calescent approaches. This result implies that introgression signal is congruent with ecological conditions making us hypothesize that it may have contributed to the transmission of adaptive important traits. Further studies evaluating the genomic regions involved in introgression and their function should be performed. Moreover, it is necessary how common this process is during *Micromeria* divergence. This way it will be possible to better understand the adaptive consequences of inter-island introgression and what is its role in the distribution of adaptive traits.

Keywords: introgression, convergent evolution, colonization, Canary islands, phylogenomics

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Evolution of reproductive barriers in sympatric Arctic charr morphs in Thingvallavatn (Iceland)

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The evolution and maintenance of reproductive barriers is a central topic in evolutionary biology as this is fundamental part of the process of speciation. As with most research on evolution, studies of speciation are difficult and the details of the underlying mechanisms are often poorly understood. Systems where closely related species or populations of the same species that have undergone adaptive divergence, come into contact are natural test beds for research on this topic. The Arctic charr (Salvelinus alpinus) of lake Thingvallavatn, Iceland is ideally suited for such studies. The lake was formed at the end of the last glacial epoch just 11-10 thousand years ago and despite its young age it now harbours four morphs of Arctic charr whose distinct variation in life history characteristics, behavior and trophic morphology suggest rapid adaptive diversification, possibly followed by, or causing build-up of reproductive barriers. In this project we focused on the two smallest morphs: a planktivorous (PL) and small benthic charr (SB), which have diverged along the limnetic (open water)- benthic (lake bottom) ecological axis. The central hypothesis underlying our investigation was that reproductive isolation between SB and PL charr is partly due to a strong negative selection against their hybrid offspring. In a common-garden laboratory experiment, we tested whether PL-SB hybrids differ from the pure parental morphs (PL and SB) in the distribution of personality traits and how this correlates with ecologically relevant behavioural- (feeding behaviour) and non-behavioural traits (yolk-sac shape and resorption, head morphology, growth rate). Our results show that PL-SB hybrids exhibit extreme (outside of the parental range) head morphologies. They also follow different ontogenetic trajectories, grow more slowly than the pure parental morphs and also show inconsistencies in their personality traits. These results point towards PL-SB hybrids having reduced fitness and support our main hypothesis of selection acting against hybrid offspring. These findings about reduced fitness in hybrids, combined with striking recent divergence in the system, represent key new information on early stages of speciation in this system, and thus have potentially critical implications for how lake Thingvallavatn and other such systems are managed.

Keywords: reproductive barriers, speciation, Arctic charr, adaptive divergence, Iceland

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Endemism within island ecosystems - Functional drivers of speciation

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Islands and archipelagos are considered as classic showcases to study speciation and diversification. Established approaches relate these processes to biological aspects such as phylogenies of taxa or diversity within taxonomic groups and to geographical aspects such as distances to other habitats or island size and elevation. In this study, we disentangle the patterns of endemism for single island endemics as well as for archipelago endemics at the scale of individual ecosystems. We consider ecosystems as functional units within islands that differ considerably in site conditions and processes. The aim is to achieve a better understanding on the contribution of ecosystem functioning and dynamics for the development and establishment of endemic species. The increasing proportion of endemism with elevation hints at diversifying processes within islands resulting from ecological isolation. However, ecological isolation can also become effective between ecosystems. Species are not distributed individually along spatial or ecological gradients, but organized through long-term evolved biotic interactions in communities and ecosystems. Here, we focus on plant species in the Canary Island archipelago and their attribution to ecosystems that are established on this set of islands. We calculated the spatial extent of major ecosystem types on all islands, and assigned all plant species to ecosystems for every single island. Many species have been recorded in several ecosystems, others are strictly tied to a particular ecosystem. Many species occur on several islands, some are archipelago endemics, others are single island endemics. We classify plant species into native (non-endemic), archipelago endemics, single island endemics, and alien (including invasive) species. By combining these levels of information, we construct a new view on the importance of ecosystems within islands for speciation. We find that the spatial extend of ecosystems within islands plays a minor role. Extensive ecosystems such as Canary Pine forest can host less species than the laurel forest, but surprisingly show a higher proportion of endemism. It is rather the type of ecosystem (e.g. fayal-brezal) that is linked on all islands with a high proportion of endemism. Harsh environments at the coast exhibit a high proportion of native species, but less endemics and alien species.

Keywords: archipelago endemics, biodiversity, Canary islands, plants, turnover

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Diversification analysis of a songbird lineage within a remote archipelago suggests a role for intra-island speciation

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Island endemic congeners can be sister species that have arisen through intra-island speciation following initial colonization by a common ancestor, or they may represent multiple independent colonization events. These two contrasting scenarios provide different expectations regarding the relative roles of natural selection and geographic isolation in driving speciation. However, discriminating between the two scenarios has proven difficult and demonstrating intra-island differentiation has remained elusive. The Reunion grey white-eye (*Zosterops borbonicus*) is a species complex that harbours four geographically structured forms with abutting ranges on a small and remote volcanic island, providing an interesting system to test for intra-island divergence. We generated genome-wide SNP loci using GBS (Genotyping-By-Sequencing) data from a large sample of individuals and a high-quality genome sequence for the species. Using a population genomic framework as well as phylogenetic inferences, we reconstructed the evolutionary histories of the different forms on Reunion island. We first confirmed the monophyly of the species relative to its sister species *Zosterops mauritianus*. Then, we show that the paraphyly and basal position of one of the lowland forms strongly argues in favour of intra-island divergence. Expansion analyses suggest sequential colonisations from the North to the South of the island. The marked genomic structure found indicates that gene flow between forms is limited and suggests that these forms may be reproductively isolated.

Keywords: intra island speciation, phylogeography, expansion, spatial structure, hybrid classes, La Réunion

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*Speaker

Human-driven extinctions have erased the evolutionary history of flightlessness in island birds

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While being able to fly is one of the most distinctive traits of birds, several lineages have lost this ability in some environments, such as oceanic islands. If we only consider extant species, the evolution of flightlessness appears to be extremely rare, occurring in only 38 out of more than 8500 species of terrestrial birds. However, these patterns might be biased by anthropogenic impacts, especially by human-caused extinctions on islands. Oceanic islands are peculiar for two reasons, when compared to larger landmasses. First, this is where we expect species to evolve towards flightless forms, due to the general lack of predation. Secondly, islands have the highest proportion of extinctions – up to 90% of recent vertebrate extinctions, according to IUCN. Since flightless birds are particularly vulnerable to new predators, we expect such species to be disproportionately represented amongst extinctions, making it difficult to understand how this trait has evolved if only focusing in extant species. In this study, we aimed to infer the evolutionary history of flightlessness in island colonizing lineages, by reconstructing the community of island birds worldwide before human disturbance. We compiled an exhaustive list of bird species that are known to have occurred on islands but have gone extinct since human arrival, totaling 472 species from 68 families. For those with sufficient morphological data, we estimated flight ability based on wing to hindlimb ratios. We accordingly classified 149 species as flightless or weak-flyers. These species quadruple the list of known flightless birds compared to extant species, and more than double the number of families with flightless representatives (from 11 to 27 known families). If we consider each flightless genus within an archipelago as an independent colonization by a flying ancestor, our data suggest that flightlessness could have evolved at least 100 times in the evolutionary history of birds, which is likely still to be an underestimate considering that the fossil record is highly incomplete. These findings highlight that humans, through non-random extinctions, have dramatically influenced the diversity and distribution of species and their traits, which must be taken into account when trying to understand natural macroevolutionary patterns.

Keywords: Birds, Flightlessness, Extinctions, Anthropogenic biases

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Multiple colonizations and parallel radiations of Peperomia (Piperaceae) on the Hawaiian Islands suggest context-dependent role of niche preemption in diversification on oceanic islands

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Niche pre-emption, where earlier arriving lineages may develop ecological and adaptive advantages and thus inhibit the ecological and evolutionary success of later arriving lineages, has been argued to play a dominant role in the assembly of oceanic island floras. On the Hawaiian Islands, for example, most of the iconic and species-rich groups of the archipelago (e.g., silverswords, lobeliads) are each derived from evolutionary radiations from single colonist lineages whereas many species-poor genera are derived from multiple colonization events. Here, using a molecular phylogeny of Peperomia (Piperaceae) in the Pacific, where it is one of the most species-rich angiosperm groups, we reveal a unique history of colonization and diversification in contrast to other elements of the Hawaiian flora and expectations under niche pre-emption. To better resolve the evolutionary relationships of Pacific taxa, we sequence full chloroplast genomes for half of species in the Pacific (including all native Hawaiian species), using a genome skimming next-generation sequencing approach. Using this phylogeny, which we date using a fossilized birth death model of the Piperales, we find that the Hawaiian Islands have been colonized by at least four separate Peperomia lineages from the Neotropics, with most diversification occurring relatively recently in the Pliocene. Most importantly, while the Hawaiian flora provides examples of spectacular radiations from single colonist ancestors (e.g., silverswords, lobeliads), we show that endemic *Peperomia* taxa on Hawaii are derived from radiations from two distinct colonists, the first documented case among species-rich plant groups of the Hawaiian flora. The diversification of two clades in parallel suggests that ecological release due to the paucity of large native vertebrate herbivores and the relatively open understoreys of Hawaiian wet forests may have allowed both lineages to flourish, and adds a new twist to our understanding of how oceanic island floras assemble.

Keywords: genome skimming, Pacific biogeography, diversification, oceanic island assembly, niche preemption

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*Speaker

Towards a comprehensive understanding of Oxera's island life

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Since the introduction of the island life concept by Wallace, isolated oceanic and relatively young islands have been the place to be to study and unravel evolutionary patterns among original groups within the tree of life. In these regards, the quite old New Caledonian archipelago has been relatively neglected despite hosting a world-class biome, perhaps because no definitive cases of adaptive radiation have been detected there thus far. Here we present a detailed analysis of the radiation of the genus *Oxera* (Lamiaceae) based on a multidisciplinary study including domestication, interspecific hybridization, kariology, anatomy, systematics, phylogenetics, pollination biology, ecology, conservation and population genetics. New Caledonia is the main center of *Oxera* diversification with about 33 endemic species plus a few more taxa in Papua New Guinea, Australia and Pacific islands. We have shown that *Oxera* originated from a single and quite recent dispersal event in New Caledonia about 4.5 million years ago, and has successfully established and diversified at an outstanding net rate of up to one species per million years. Establishment and rapid initial diversification of *Oxera* in New Caledonia was probably facilitated by arid conditions that may have created new biota at the beginning of the Pliocene. Concurrently, *Oxera* also underwent major shifts in pollination syndromes, dispersal modes and life forms that are now exhibited by its extant major clades. More recently, the drivers of speciation within the main clades are most likely due to allopatry and habitat shifts in relation to climatic oscillations and soil morphogenesis. Ongoing population genetic studies on several species from different clades (e.g. within the monocaulous baladica clade and especially on the *Oxera baladica* species complex) are highlighting more recent stories, while the complete genome sequencing of a taxon (*Oxera pulchella* subsp. *grandiflora*) is likely to deepen our outstanding of the past demographic history of several species and/or clades. *In fine*, we hope the results will be of interest for the conservation of the most critically endangered *Oxera* taxa.

Keywords: Oxera, New Caledonia, Lamiaceae, radiation, niche shifts, demographic history

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*Speaker

Unraveling the stages of ant diversification in Madagascar

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Evolutionary radiation typically involves the divergence of lineages across geographic, ecological, and phenotypic spaces, but diversification may not happen along these dimensions simultaneously. Indeed, both theory and empirical studies have suggested that radiation may occur in stages, for example with diversification first occurring along climatic gradients and later along body size (or vice versa). This may reflect evolutionary "paths of least resistance"; the relative ease in which species can cross dispersal barriers, evolve across morphospace, and adapt to different climates. However, it is still unclear whether radiations are generally staged, and, if they are, whether the ordering of the stages is general across taxa or highly idiosyncratic. Here, we assemble an unprecedented dataset for ants encompassing the taxonomic, geographic, phylogenomic, and phenomic dimensions of ant biodiversity in Madagascar to analyze the dynamics of diversification across five major ant radiations on the island (total ≈ 500 species). As an isolated mini-continent, Madagascar is both a model system for comparative analysis of diversification and also a critically important region for conservation. Building upon 25 years of intensive ant biodiversity inventory across Madagascar, we analyze the distribution of species across the main geographic regions of the island, across ecoclimatic gradients, and in 3D morphospace as quantified by X-ray microcomputed tomography and 3D geometric morphometrics. Phylogenomic reconstructions show that a small handful of colonizing lineages seeded massive radiations in the five focal genera after colonization. In general, we found evidence of staging in each group, as radiation proceeded along certain dimensions early and others later, rather than a synchronous accumulation of diversity in all dimensions. However, the ordering of these stages varied considerably among taxa, with morphology diversifying first followed later by climatic tolerance in some taxa, while in others the reverse was true. These differences were partially understandable, for example one genus lacks flying queens and showed much more geographic structure to the radiation, but in many cases are enigmatic. These results shed light on the dynamics of adaptive radiation in this biodiversity hotspot, while highlighting questions about why the adaptive potential of different lineages varies so considerably across dimensions of biodiversity.

Keywords: adaptive radiation, ants, Madagascar, diversification, biogeography, morphology

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[*] Speaker

Unraveling the history of *Apis mellifera* in the islands of the South-West Indian Ocean: what we have learned from genetic, genomic, morphometric and ecological approaches

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Honeybees are present on all islands of the South Western Indian Ocean (SWIO), including Madagascar and three surrounding archipelagos (the Comoros, Seychelles and Mascarenes). If *Apis mellifera unicolor* is indubitably an African subspecies endemic to Madagascar, its relationship with insular honey bee populations from this hotspot of biodiversity is misunderstood and its ecological role in natural ecosystems still poorly documented. In such a context, the evolutionary history of the species in the SWIO is pertinent to explore. The aims were to (i) characterize the genetic origins and diversity of the insular populations (ii) test whether morphological and genetic divergences among populations correlate and (iii) investigate the ecological role through the study of biotic interactions with the native flora. In collaboration with regional partners, a dataset of more than 4 000 colonies sampled in Madagascar and the 9 surrounding islands were considered for genetic, morphometric and genomic analyses. Mitochondrial screening indicated that insular populations belong to one private African sub-group, but also revealed recent human importation of European subspecies in the Mascarene Islands (Mauritius, Rodrigues, La Réunion). Nuclear DNA analyses highlighted significant genetic differentiations among insular populations from this African sub-group, suggesting ancient colonization events. When confronted, the patterns of genetic and morphological diversification observed were highly congruent both at the inter- and intra-archipelago scales. In Reunion, whole genome sequencing of individuals (n=36) showed admixture between African and European lineages, with however a higher level of *A. mellifera unicolor* mitotype. Results provide insights into the long- term consequences of introducing exotic specimens on the nuclear genome and indirectly on the morphology of locally adapted populations. Ecological surveys conducted in natural forest ecosystems from Madagascar and La Reunion confirmed the generalist foraging behavior strategy of *A. m. unicolor* and revealed a significant preference for native floral species. All together, these results shed light on the original diversity of the honeybee in the SWIO and the need to preserve it.

Keywords: adaptation, *Apis mellifera*, honeybee, insects, Madagascar, molecular evolution, pollination

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Evolution of dengue viruses on islands

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Dengue virus is an emerging infectious mosquito-borne disease that has been expanding worldwide in recent decades. Currently over 3.5 billion people are estimated to be at risk to infection, although a disproportionate number are from low-income tropical populations. Many islands are affected by dengue, either supporting dengue endemically or subject to periodic introductions through traveling humans. *Aedes aegypti* is the primary vector, although *Aedes albopictus* and other relatives are potentially important secondary vectors. Dengue, as a fast-evolving RNA virus, has the ability to adapt rapidly to new ecological opportunities. To understand how dengue viruses evolve in different island systems and identify the major drivers that might lead to endemism, we sequenced viruses for their complete genomes and analyzed evolutionary patterns in a phylogenetic framework. Our findings suggest that higher virus population sizes and resultant genetic diversity are important for dengue establishment and long-term evolving populations. Both endemic and introduced dengue can be associated with severe disease epidemics or outbreaks. These results have major implications for understanding how dengue circulation and its sources through human travel impact diseases on islands.

Keywords: borne, dengue, epidemic, infectious disease, mosquito, vector

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The eco-evolutionary feedbacks of why island forms so often differ from their mainland counterparts

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Closely related island and mainland forms of the same species often differ in morphology, life history, diet, and behaviour. In cases where the mainland form has colonised multiple different islands, patterns of independent phenotype evolution on each island are often remarkably similar, providing compelling evidence that evolution is often repeatable. Why is this? In this talk I will present a general framework that describes why release from predation and/or interspecific competitors can generate repeatable patterns of evolution. I will illustrate the theoretical framework with observations from a number of island systems. My approach uses evolutionarily-explicit structured models that capture eco-evolutionary feedbacks of interacting species, with analyses of these models demonstrating the circumstances under which adaptation to an island environment is likely to generate repeated patterns of evolution. My results help explain why island species so often differ from their mainland counterparts, and once again demonstrates the importance of islands in generating general ecological and evolutionary insight.

Keywords: Insular syndrome, island rule, intraspecific competition, vertebrates

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Island versus mainland evolution of a ‘great speciator’: contrasting patterns of morphological diversification in the white-eye radiation

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Islands and continents have had profound effects on how biodiversity is shaped. While evolutionary processes are predicted to follow different patterns in island and mainland radiations, the extent to which these geographical contexts influence evolutionary trajectories remains poorly understood. This is in part because few studies have focused on species-rich groups that are highly dispersive, and which can colonise continents and archipelagos over comparable timeframes. To address this knowledge gap, this talk will focus on *Zosterops* (white-eyes), a highly diverse, yet cryptic songbird genus that has been lauded as a ‘great speciator.’ Focusing on taxa from Africa-Arabia and associated islands, including the archipelagos of the western Indian Ocean and Gulf of Guinea, a comprehensive multi-locus phylogeny for the region was generated harnessing field and museum collections. The resulting hypothesis revealed exceptionally recent colonisation of the mainland (1.3-2.78 Ma) from Asia, with subsequent independent colonisations of islands, as well as highlighting substantial hidden diversity. Trait data from museum specimens was also generated and combined with the phylogeny using various comparative methods, allowing hypotheses of morphological evolution to be tested in a radiation spanning different geographic scales. Although an early burst and slowdown pattern of lineage accumulation for this radiation was identified supporting a previous study, this is coupled to apparent convergence on particular phenotypes. An absence of an adaptive signal of phenotypic evolution in *Zosterops* is not, however, unsurprising given the overall remarkably cryptic phenotypes exhibited in this genus. Notably, this phenotypic signal is shown to be strongly driven by mainland taxa, which is suggested to have been caused by niche divergence through repeated speciation between highland and lowland habitats, in which phenotypes appear to be highly constrained within particular environments. In contrast, island birds are generally not distinguishable from a random-walk model and have repeatedly expanded into novel areas of morphospace. It is suggested the different trajectory of evolution in insular *Zosterops* radiations arises from a lack of species competition, with an increase in ecological opportunity thereby providing a release to phenotypic constraints experienced by continental taxa.

Keywords: Disparity, through, time, cryptic species, diversification, niche divergence, competition

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[*] Speaker

A meta-analysis of mainland and island populations suggests a general isolation syndrome affecting traits, demography, and genetic diversity

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Oceanic (geographical) islands, due to their geographically isolated evolutionary histories and the general paucity of interacting populations, are extreme cases of geographic isolation. Populations of plants and animals on islands are subject to strong selection pressures that lead to important changes in their life history strategies, when compared with their mainland counterparts. While the island syndrome may be an extreme case of insularity, isolation syndrome can also emerge across various ecological islands on the mainland. We assessed the generality of the biogeographic mechanisms of isolation-by-distance and isolation-by-environment by developing the "GEOPOP: Geography of Populations" database, which currently contains 13500 population-level measurements of genetic, morphological and demography traits (7529 entries from oceanic islands and 6042 entries from the mainland) for 2035 georeferenced populations of plants and animals published in 160 studies. Using this database we extended the "island syndrome" concept to the "isolation syndrome", and tested to what extent the "isolation syndrome" is a general biogeographic driver of trait variation in mainland and island systems. Specifically, we tested to what extent differences in the mean and variability of traits, demography, and genetic diversity of populations were predicted by the geographic distance and the environmental distance between populations, and whether the effect of the isolation by distance is stronger within island systems. Our preliminary results support predictions from the "isolation syndrome", i.e. higher differentiation between populations with increasing geographic and environmental distances between populations. While these effects were found in both island and mainland systems, island populations had higher differentiations between populations when compared to mainland systems, highlighting the clearer isolation effects in island systems. The isolation-by-distance underlying the island syndrome is a particular case of the general isolation-by-distance biogeographic mechanism. Expanding the "island" concept from isolated physical land or water bodies to more general, ecological-evolutionary processes paves the way towards a conceptual unification of the phenomenon of insularity across marine and terrestrial systems of ecological islands.

Keywords: ecological islands, environmental distance, fragmentation, GEOPOP, insularity, island syndrome

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[†] Speaker

Plant mating systems on islands

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In the 1960's, as part of the interest for island biology, one of main interest of botanists was to analyze plant mating system syndromes on islands. An influential model for interpreting mating system patterns is based on pollination processes and has been popularized under the verbal model " Baker's law " (Baker, 1955). This "law" proposes that 'with a self-compatible individual a single propagule is sufficient to start a sexually reproducing colony, making its establishment much more likely than if the chance growth of two self-incompatible yet cross compatible individuals sufficiently close together spatially and temporally is required' (mate availability). A second line of argument proposes that 'self-compatible flowering plants are usually able to form some seed in the absence of visits from specialized pollinating insects, which may be absent from the new situations' (pollinator availability). This model, addressing not only mating systems on islands but more generally of colonizing species (Baker and Stebbins, 1965) has been, since its publication controversial. In 1966, Carlquist argued that 'if dioecious stocks immigrated to the [Hawaiian] islands, Baker's Law must be in part abandoned'. More than fifty years later, estimates of plant mating system has accumulated, in particular thanks to the intensive use of molecular markers. In the recent years, theoretical models have also made predictions about the evolution of colonization ability and mating system, with mixed support for Baker's law (Cheptou, 2012). In this talk, I will present the recent empirical results and theoretical predictions addressing the link between colonization and mating system and how it can help to think about mating system syndromes on islands. The results suggest that such island syndromes may not be unequivocal. Clarifying ecological scenarios are key to interpret plant mating systems on islands.

Keywords: Baker's law – island syndrome – plants – data, theory

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*Speaker

The biogeography of insular size evolution: the effects of isolation, island area and age on size changes in island plants

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Recent evidence suggests that, like island animals, island plants evolve in repeated and predictable ways on isolated islands. Of these changes, the most frequently is the evolution of island dwarves and giants (i.e. size changes). However, to date, no study has demonstrated how size changes in islands plants vary with geography. I documented size changes in plant species widespread across ten islands off of the east coast of New Zealand. I then asked how the strength of these changes varied as a function of isolation, island area, and island age. Overall results were consistent with the island rule in animals, that is, large plant dwarfism and small plant gigantism. However, the magnitude of size changes was not consistent among islands; suggesting that geography plays an important role in the evolutionary trajectory of island plants.

Keywords: loss of size diversity, insular evolution, size changes, gigantism, dwarfism

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*Speaker

Evolutionary convergence in the flora of New Caledonia: correlated evolution and environmental contingencies of monocauly

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Evolutionary convergence, i.e. the rise of similar trait attributes among distantly related lineages, is a symptomatic island syndrome. Many tropical islands host remarkable cases of evolutionary convergence in plant forms and functions, among the most famous being secondary woodiness. In New Caledonia, an insular biodiversity hotspot in the Southwest Pacific, secondary woodiness is virtually lacking. Botanists who studied the flora, however mentioned the pervasive presence of monocaulous (unbranched) woody species in many distinct lineages, potentially illustrating a previously uninvestigated case of convergent evolution. Here, we study the evolutionary history of monocaulous species throughout the phylogeny of the New Caledonian woody genera. Using herbarium data, extensive field work and a compilation of the literature, we listed monocaulous species and scored six life-history and two environmental traits for 2114 New Caledonian woody self-supporting species. We constructed a phylogenetic supertree at genus level to investigate minimum number of times monocauly has evolved, phylogenetic signal and evolutionary correlates of monocauly in the island. We found at least 31 independent evolutionary events leading to monocauly, with 182 monocaulous species belonging to 41 genera, 30 families and 15 orders. This repeated evolution of the monocauly is revealed as a remarkable case of convergence in insular environments. Monocaulous species conform to few architectural models. The habit showed a nonrandom distribution over the phylogeny suggesting some prerequisites facilitating its evolution. Monocauly evolved preferentially in rainforest and on ultramafic substrate and triggered the evolution of both cauliflory and marked rhythmic growth, but no preadaptation was identified. Environmental contingencies explaining this notable convergence are suggested to involve rainforest structure and historical climatic stability, ultramafic (nutrient-poor and toxic) substrates and long-term absence of browsers. Finally, we ask whether the convergent evolution of monocauly in New Caledonia results from the loss of branching in the different lineages, as suggested by the few phylogenetic data available. Notably, secondary woodiness is also often associated with the evolution of unbranched rosette trees on islands, conforming to the Holttum or Corner architectural models. Are branches lost on islands? If so, why? Convergent evolution in plant architecture could represent an overlooked insular syndrome.

Keywords: convergent evolution, environmental contingencies, disharmony, monocauly, architecture

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[†] Speaker

Understanding biodiversity dynamics by applying eco-evolutionary simulation models to insular systems

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Assessing mechanisms underlying biodiversity patterns requires appropriate study systems and methods. Islands offer ideal study systems, having sparkled influential theories in both ecology and evolution. Recent advancements in mechanistic models for biodiversity dynamics are providing the tools to manipulate factors and processes at a spatiotemporal scale that is impossible in real-world experiments. We aim to promote the application of eco-evolutionary simulation models in insular settings to understand biodiversity dynamics in general. We present three experiments using spatially-explicit, eco-evolutionary, individual- and population-based models of plant metacommunities applied to oceanic islands to address different questions concerning biodiversity: 1) how genetic and ecological traits interact to generate different diversification dynamics; 2) what factors facilitate species invasions; 3) what are the effects of isolation on species diversification. In the experiment contrasting genetic and ecological traits, we found that a high degree of gene linkage causes lineages to show more niche conservatism, whereas low linkage results in populations with more flexible capabilities in ecological adaptation. In the experiment contrasting different scenarios of propagule pressure, disturbance and species pool to assess island invasibility, propagule pressure showed the strongest positive influence on the success of plant invaders. In the experiment contrasting isolation scenarios, we found that abiotic (e.g. distance, propagule pressure) and biotic (e.g. dispersal ability and specie spool size) components of isolation increased the number of diversifying lineages and of species per diversifying lineage. These examples illustrate aspects of eco-evolutionary dynamics that are difficult to address in real-world systems, but that can be tackled with mechanistic models. Considering that there have been an increase of mechanistic models for large spatiotemporal scales in general, we believe that applying those models to island-like systems will provide valuable insights and will speed up our understanding of complex process interactions governing biodiversity dynamics.

Keywords: mechanistic simulation models, ecoevolutionary feedbacks, biodiversity research, ecological theory, island floras

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Interdisciplinary Island Studies

Contents

Detecting burnt scars from space: A case study of the January 2019 wildfires along the eastern flank of Piton de la Fournaise Volcano, La Réunion

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Like many other tropical environments, La Réunion island hosts a vast variety of indigenous and endemic species. This is not only due to its geographical isolation in the Indian Ocean, but also because of the rich diversity of natural habitats, and the existence of many micro-climates. The island is of volcanic origin and the landscapes of its eastern part are, until today, continuously transformed by the active Piton de la Fournaise Volcano. Besides frequent volcanic eruptions that produce basaltic lava flows, wildfires also threaten the vegetation along the volcano's flanks. A major wildfire occurred between 20 and 27 January, 2019, in the Grand Brûlé, an area characterized by extremely steep slopes, dense vegetation and seaward ground movement of $\approx$3 cm/yr that is caused by gravitational edifice spreading. The area affected by the fires was estimated to roughly 2000 ha by the *Service Départemental d'Incendie et de Secours (SDIS)*. We used Synthetic Aperture Radar (SAR) imagery collected by the European Sentinel-1 satellite in order to more accurately map the extent of the burn scar by applying two main techniques: a) a change detection technique comparing the backscatter intensity before (2019/01/17) and after (2019/01/29) the wildfires, and b) SAR interferometry, a technique that allows tracking surface changes over time by calculating the difference between the post- minus the pre-event interferometric coherence in order to estimate the areas of vegetation loss. Our results suggest that a minimum of 1500 ha of vegetation were lost during the fires. Ground investigations during and after the event allowed for the identification of two main types of fire dynamics: a) In densely forested areas, mainly the ground vegetation was destroyed, while larger trees survived, producing characteristic discontinuous patterns in satellite imagery, b) Mosses and lichens covering younger lava flows burned entirely, appearing as distinctive continuous patterns in satellite imagery. Our analysis helped mapping and characterizing the total area affected by the January 2019 wildfires along the eastern flank of Piton de la Fournaise Volcano, and demonstrates the applicability of SAR satellite imagery for rapid mapping of burnt scars.

Keywords: La Réunion, wildfire, biodiversity, SAR remote sensing, coherence

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Spatial footprint of natural disasters: opportunities and challenges for remote sensing in the south-western Indian Ocean

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The concept of spatial footprint is classically used to describe the geographical impact of a natural event on landscape. From the perspective of remote-sensing, this footprint can be assessed by implementing methodologies to detect changes in the spectral signature of a pixel or an object contained in multiple dates or time-series images. Since the 2000s, various phenomena such as forest fires, hurricanes, floodings or coral bleaching have been monitored using change detection approaches throughout the western indian ocean, including La Réunion. The methodologies and results of these studies are presented here highlighting their contribution in the assessment of impacts on insular territories. On the basis of results obtained locally and regionally (projects RENOV-RISK Impact, TAIMPO, Becoming,...), we introduce the fundamentals and future opportunities of such methods in the context of Big Data (large volume of data, at high temporal and spatial resolutions) with national and international programs such as THEIA, GEOSUD, Kalideos or Copernicus. These programs favor the free distribution of earth observation data, products and methodologies from high-resolution optical and SAR sensors (Landsat, Sentinel 1 and 2...). We will evidence *(i)* the importance of developing generic preprocessing chains and producing standardized products, regardless of acquisition specifications, to be used for temporal analysis dedicated to landscape evolution monitoring, in various geographical contexts, and for a large range of thematic applications, *(ii)* the interest of building generic change detection toolboxes through the production of simple standardized products (NDVI, NDWI, IB on optical data and normalized difference on SAR), to widen the applications based on earth observation data and make such technologies available to larger user communities.

Keywords: natural disasters, change detection, spatial footprint, SAR remote sensing, optical remote sensing

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Anoles & Drones: Revealing controls on distribution and microhabitat use of Anolis lizards in a changing island landscape using emerging remote sensing technologies

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In these times of rapid environmental change and species extinction, understanding the drivers governing species' abundance and distribution is more important than ever. The goal of this work is to further our understanding of what drives variation in species' abundance and microhabitat use through space, particularly in the context of rapid land cover change and biological invasion. Using the little explored anole (*Anolis*) fauna of the Honduran island of Utila. Here, we test theory linking sub-canopy thermal conditions to canopy density, evaluate the capacity of unmanned aerial vehicles (UAVs) to predict fine-scale heterogeneity in thermal habitat quality in forest, plantation, mangrove and urban environments, and evaluate thermal implications for endemic and invasive anoles. Pilot work coupled operative temperature data (morphologically accurate 3D models fitted with data loggers), with UAV derived NDVI measurements. Results reported a significant relationship ($P < 0.001$) that as spatial heterogeneity in NDVI increases, so does the standard deviation of operative temperature. Therefore, measurements of canopy structure from UAVs have the potential to provide fine-scale predictions of spatial heterogeneity of thermal habitat quality for animals at greater resolutions than can currently be obtained from existing microclimate datasets and methods. Pilot work also revealed a distinct habitat preference in the endemic *Anolis bicaorum* and has noted an increased range and habitat usage of the invasive *Anolis sagrei.* To evaluate thermal suitability of each Utila's habitats, the number of hours that operative temperature was within Tbreadth (range of temperatures where animal can reach 80% of its maximal performance) for each anole species was calculated. Results indicate most habitats are more thermally suitable for *A. sagrei* than *A. bicaorum*, apart from forest which is too cool for *A. sagrei.* Unexpectedly, thermal suitability of urban plots was not substantially higher for *A. sagrei* than *A. bicaorum.* Therefore, distribution of Utila's anoles are not solely driven by thermal suitability, future work will evaluate the role of predation, food resources and habitat structure. This work allows us to improve our understanding of Utila's *Anolis* fauna, promote its conservation and demonstrate how emerging technologies can help us understand and preserve the natural world.

Keywords: conservation, remote sensing, biological invasion, microhabitat, thermal ecology

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An open network to monitor marine environment and species

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Data acquisition and monitoring of marine species and their environment is a major challenge in ecology and conservation. Marine scientific instruments (beacons, tags, buoys) are generally very expensive tools that do not allow large scale and numerous monitoring. Various research projects are being carried out to provide connected instruments at a reduced cost. For this purpose, free electronics and transmission methods using the Internet of Things technology have been developed to provide open access data. For the moment, we have been able to develop tags to track the movements of marine turtles in a network of ground stations and buoys recording physical information (temperature, wave height). Tags cost less than 100 € and buoys cost about 300 € , which is almost 10 times less expensive than commercial instruments. The instruments are developed so they are resistant to extreme conditions of tropical remote islands, autonomous in energy, and being able to transfer data remotely without a cell or internet network around. These initial results show the possibility of establishing a large-scale network for monitoring environmental conditions and marine animals at reasonable costs. The codes and hardware being free, this allows everyone to add or customize the specifications of the objects according to the scientific questions asked.

Keywords: buoy, LoRa, low cost, tag, turtle

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*Speaker

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Marine sponges from Indian Ocean, a highly promising source for the discovery of novel bioactive compounds to fight against ageing and age-related diseases

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Ageing is commonly defined as the accumulation of diverse deleterious changes occurring in cells and tissues with advancing age that are responsible for the increased risk of pathologies such as Alzheimer's disease, cardiovascular diseases, neurodegeneration or cancers. As the population of developed countries is ageing, the prevalence of a variety of age-related diseases is increasing. In order to counteract this major healthcare challenge, marine natural products represent an extraordinary reservoir of structurally diverse bioactive metabolites which may present anti-ageing properties and offer pharmaceutical, cosmeceutical or nutraceutical applications. Taking into consideration the aforementioned issues, the H2020 European project TASCMAR explores marine invertebrates and symbionts from under-investigated marine biodiversity hotspots and develops innovative approaches for the discovery and production of compounds with anti-ageing activity. The Chemistry Laboratory of Natural Substances and Food Sciences (LCSNSA, University of La Réunion) located at Réunion island is involved in this ambitious research program and this communication will therefore provide an outline of its contribution to TASCMAR. We collected a total of 112 sponges from Mayotte and Rodrigues (Indian Ocean). The crude extracts of the samples were submitted to a biological evaluation against a wide range of different targets involved in ageing or age-related diseases. These targets include catalase, sirtuin 1, CDK7, proteasome, Fyn kinase, tyrosinase and elastase. Twenty nine crude extracts have shown promising results. The chemical investigation of these 29 extracts for the discovery of molecules with anti-ageing effects will be discussed.

Keywords: age related diseases, anti ageing activity, marine sponges, novel bioactive compounds, TASCMAR

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Monitoring of fish communities and benthic habitats from unbaited underwater video techniques with applications to Indian Ocean conservation and fisheries management challenges

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In coastal areas, anthropogenic pressures are intense and spatially organized, and benthic habitats are heterogeneous, both locally and at larger scales. Monitoring-based assessment of fish communities and biotic habitats in such areas generally suffers from a poor spatial replication, which makes the area-wide assessment of key biological components, such as fish communities and benthic habitat, quite challenging. This paper presents the data obtained from unbaited remote underwater video system designed to address such challenges (STAVIRO) developed from 2007. The STAVIRO is a standardized methodology for field work, for analysing footages and for assessment. This system enables monitoring and studying shallow biodiversity, mostly in coastal areas (between 0 and 70 m), providing observations of habitat and vagile macrofauna. The rotation provides a panoramic view without distorting image due to wide angle. Not requiring divers, nor a scientific background on the field, many observations can be collected, ca. 20-25 stations per day on a small boat with two systems, allowing to survey potentially vast areas on both soft and hard substrates, and to replicate observations, using a standardized protocol. The STAVIRO results from EPICURE project allowed us to estimate the health status of fish communities at Geyser bank, and more specifically the main commercial fish species targeted at the onset of the artisanal hook fishery from Mayotte Island. The large species of serranidae, lutjanidae, lethrinidae and carangidae constituted the bulk of the annual catches landed in the years 1990. Depending species and sites, results highlighted a) unbalanced stocks in size distribution; b) low abundances levels, even cases of rarefaction of the largest targeted species (total length $>$ 60 cm); and c) significantly higher abundances for gregarious species with a maximum size generally less than 60 cm. These results are obvious signs of overexploitation for the major commercial great species targeted by fisheries. They will be helpful for supporting forthcoming decisions related to fisheries management, and they provide a baseline for future assessments and for research.

Keywords: underwater video system, fish communities, reef habitats, fisheries assessment, fish monitoring

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Isolated Indian Ocean islands: little POPs, some heavy metals, and much plastics

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Isolated coral reef islands in the Western Indian Ocean (WIO) collect marine debris from distant sources. We traced plastics and other items found on Agalega and St. Brandon's to have originated in Southeast Asia and the Arabian Sea. Analyses of the plastics revealed appreciable concentrations of persistent organic pollutants (POPs) and mercury. We have also found plastics in nests of Brown Noddies and Sooty Terns. However, it does not seem as if these pollutants actually transfer into marine bird eggs. Tern eggs from Rodrigues for instance, contain some of the lowest POP concentrations anywhere in the world. On the other hand, some of the corals from St. Brandon's contain higher concentrations of some metals than corals from elsewhere in the Indian Ocean. The ecotoxicology of WIO islands remains understudied. Interactions of biota with climate change, ocean acidification, and a probable increase in pollutant and plastics releases, may pose a significant threat to coral reef islands.

Keywords: pollution, plastics, birds, coral

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Unsanctioned imports: the problem of plastic debris in small island states

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Plastic production has increased from 1.7 million tons in 1954 to 335 million tons in 2016, with approximately 8 million tons of plastic entering the ocean annually – largely as a result of mismanaged waste. A study of the world's waste management shows that the Indian Ocean is fringed by countries with 100% mismanaged waste. This plastic is transported by currents and winds throughout the world's oceans, with the end point for some being remote islands in biodiversity hotspots. The Seychelles is an archipelago of over 115 islands, stretching over 1.4 million km2 of the Western Indian Ocean. Vast quantities of marine plastic pollution have accumulated along the coastlines of these islands and this is now affecting some of the Seychelles' endemic and endangered wildlife. Increased understanding and effective management of this is greatly needed. Surveys to assess quantity, composition, accumulation rate, attached biota, and removal effort were conducted alongside the Aldabra Clean-Up Project in March 2019, an international initiative to clear Aldabra Atoll UNESCO World Heritage Site of accumulated waste. I will present on the total waste found to have accumulated on Aldabra, total waste removed, the effort per unit of waste removed, removal costs, and seasonal accumulation rates. Initial surveys show that consumer items on the north coast and fishing gear on the south coast dominate composition. Additionally, I will present the proportion of debris arriving with attached biota and the types of biota recorded. Islands might only produce a small amount of waste internally, and yet receive huge amounts of waste from other countries – these island nations are therefore unwillingly importing large amounts of waste, which must then be managed. The threat plastic pollution poses to even remote and otherwise well-protected islands is vast and will require considerable allocation of resources to mitigate. The composition of waste found on Aldabra demonstrates that whilst reducing land to sea pollution pathways must be a priority, the fisheries sector must also greatly reduce their marine pollution. Lastly, island managers must consider the potential impact that increased species connectivity via plastic pollution will have on island ecosystems.

Keywords: plastic pollution, rafting biota, threat management, Protected area, Seychelles

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*Speaker

Marine Ecology

Contents

Long-term monitoring of coral reefs in the Mozambique Channel (Indian Ocean): paving the way towards integrative regional management

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Understanding the functioning of coral reefs and their resilience to disturbance requires long-term studies of sites subjected to contrasting anthropogenic pressure but similar climatic forcing. A better understanding of the connectivity between marine populations is also essential for management. In this context, the SIREME program (Monitoring and Inventory of coral reefs of Mayotte and the Iles Eparses) was conducted in the Indian Ocean to measure the state of health of coral reefs and evaluate the connectivity between islands in the Mozambique Channel. The main coral reef components (corals, fish and microplankton) were monitored in Mayotte and Iles Eparses using underwater visual census techniques and habitat were mapped through satellite and field data. The degree of connectivity between island reefs was assessed in genetic studies and hydrodynamic simulations. Monitoring indicators were proposed to estimate the effectiveness of management measures. In Mayotte, fish biomass (2) has declined drastically over the last decade (high fishing pressure), in particular at higher trophic levels. Nevertheless coral and fish diversities were high, as was the total species richness, due to favourable geological and hydrodynamic conditions in the northern Mozambique Channel. In the Iles Eparses, the coral reefs were stunning, reflected either by high coral cover (e.g. Europa) or the dominance of "living corals-CCA" compared to soft algae (e.g. Glorieuses). A high biomass (up to 10 times higher/Mayotte) and proportion of predators and large specimens characterized these fish communities. Connectivity between islands differed according to species studied. Hydrodynamic modeling highlighted strong inter-connectivity between the reefs of the Mozambique Channel, particularly Glorieuses and Mayotte, favouring their resilience. However, more isolated islands such as Europa, located to the south, may be more vulnerable to repeated bleaching events.

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Keywords: biodiversity, connectivity, coral reefs, indicators, management

Functional vulnerability in Western Indian coral reef fishes: indicator species and conservation priorities

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Due to limited resources and the high species richness observed in coral reefs, scientists and managers have to focus monitoring activities on a subset of taxa. Here, in the context of the SIREME project (10th EDF Indian Ocean), we investigated the functional structure of wilderness coral reef fish assemblages of the Western Indian Ocean (WIO) : Mayotte and the Îles Éparses, Mozambique Channel. By studying the relationship between function importance and vulnerability, we illustrate an approach useful to characterise particular species and populations as conservation priorities. We evaluated the functional diversity (FD) and vulnerability of fish assemblages in various coral reefs in the WIO. Fish species were described using six functional traits. Functional entities (FEs) were defined as unique combinations of these traits, with each species belonging to a single FE. We used biomass as a proxy for measuring the importance of FEs and functional vulnerability using the distribution of species, individuals and sensitivity to fishing across FEs. By combining information on vulnerability and importance, we identify FEs – and thus species – that are priorities for future monitoring and conservation actions. Using beta-diversity measures, we evaluated the congruence of functional conservation priorities across assemblages. A total of 398 species distributed among 162 FEs were identified. We found that the distribution of species and individuals within these FEs was uneven, and that many FEs appear vulnerable to the loss of species or individuals. The beta-diversity of priority FEs was found to be moderate or high across the six assemblages. The functioning of reef fish assemblages in the WIO is highly vulnerable to the loss of species and individuals. Because priority FEs are dissimilar across islands, management measures should be adapted to each system. We show that the approach adopted in this study is useful for identifying priority species for conservation and management purposes in coral reefs.

Keywords: conservation priorities, coral reefs, functional diversity, functional vulnerability, Îles Éparses, Western Indian Ocean

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Energy packing of reef fish communities in isolated oceanic islands

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Underwater, tropical oceanic islands are generally portrayed as oligotrophic environments, occasionally subsidised in energy from different sources, for instance guano from land, or nutrients from upwelling events. However, we still lack (1) quantitative estimates of the amount of energetic subsidise entering marine communities in isolated tropical oceanic islands, and (2) understanding of the potential drivers for these subsidise. Here I use a theoretical approach based on first principles of energy-mass balance to quantify the fraction of reef-fish carbon consumption that is likely to be dependent from allochthonous sources in oceanic islands all over the globe. For that, I use a meta-analysis of fish respiratory rates combined with a recent global dataset of reef-fish community structure, and satellite-derived data. Preliminary results indicate that oceanic islands in the Tropical Eastern Pacific and central Atlantic are heavily subsidised, primarily through trophic levels that utilise plankton as a major food source. In this talk I will discuss how much of this subsidise can be explained by a number of biotic and abiotic factors, for the entire community and different trophic groups.

Keywords: metabolic theory, coral reefs, energetics, respiration, carbon cycle

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*Speaker

Multi-scale effects of environmental stress on reef fish communities of the Galapagos islands

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Ecological communities on islands are composed of subsets of species pools from colonizing "mainland" sources. On oceanic archipelagos such as the Galapagos Islands, marine faunas derive from multiple biogeographic sources and occupy a broad range of ecological niches. It is unclear which biogeographic and ecological traits will confer population stability as environmental stressors become more extreme with climate change. We used a 6-year monitoring program of the wide oceanographic variation and relatively pristine fish communities of the Galapagos islands as a model system to study ecological outcomes and population dynamics in response to variation in environmental stress occurring at different spatio-temporal scales. In response to a local, high-frequency stress (wave exposure), we found that speed of locomotion dictates the ability of herbivores to navigate high wave exposure. Fast-moving herbivorous fishes alternate between feeding patches and refuges from stress at a higher frequency than the return time of extreme wave-induced flow speeds. At these small (ecological) spatio-temporal scales, mobility is the factor that best predicts a species' ability to continue feeding and exerting top-down control of benthic communities under periodic environmental stress. Tracking reef fish population trajectories over 6 years in response to a regional, low-frequency stress (El Niño events), we compared the predictive capacity of factors directly related to physiological tolerance to climate change (biogeographic and phylogenetic effects) with traits indirectly related to the effects of climate change on limiting resources (trophic and habitat effects). Planktivores were extremely susceptible to population declines during El Niño, but showed remarkable resilience by bouncing back during the subsequent La Niña one year later. Species derived from Indo-Pacific and Panamic lineages were also mildly favored during El Niño relative to Peruvian species. Our results suggest that mobility is a key behavioral trait for stress avoidance in the short term, and that limiting resources (such as planktonic food) are a better predictor of the long-term response of marine fish populations to climate change than proxies of physiological tolerance to changing environmental conditions.

Keywords: climate change, community ecology, El Niño, population dynamics, reef fish

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A continent-island model of gene flow in a marine fish from the Western Indian Ocean

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The continent-island model of gene flow has been central to better understand the impact of migration in island populations, but it has rarely been applied to marine species. The meridional part of the Western Indian Ocean (WIO) is characterized by a patchy distribution of reef habitats that matches a continent-island model, with a large network in the Mozambique Channel and peripheral habitats representing independent ecoregions (Mascarenes). Here, we use the cordonnier Siganus sutor inhabiting reef flats and lagoons of the region, to explore a special case of the continent-island model with bidirectional gene flow. Using multiple markers and samples throughout the WIO, we confirmed the existence of two populations in the cordonnier, one large in the Mozambique Channel and one in the Mascarene that probably diverged during the Last Glacial Maximum. Despite the main westward oceanographic circulation, the gene flow occurred predominantly from The Mozambique Channel to the Mascarene, as expected under a continent-island migration model. Modelling and simulations confirm that migration has a large effect on the allele frequency of the island population while the continent population stays intact when assuming bidirectional gene flow and a sufficiently large difference in population sizes between the continent and the island. These observations bring new lights on the patterns of bidirectional asymmetrical gene flow frequently observed in the literature.

Keywords: Asymmetric gene flow, marine biogeography, continent, island model, dispersal, environmental factors, genetics

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The Alcyonacea (Octocorallia) on coral reefs at Europa Island: How are they connected with other soft coral communities in the Mozambique Channel?

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The soft corals (Alcyonacea: Octocorallia) on reefs around Europa Island were surveyed in 2016. Alcyonacea were sought and collected within all the reef habitats at Europa and their relative abundance was visually recorded as being rare, occasional, common or abundant. The colonies were photographed underwater before sampling and the samples were fixed for identification and storage in the Steinhardt Museum of Natural History in Tel Aviv. Since Europa Island is remote and isolated, connectivity with other alcyonacean communities in the Mozambique Channel was investigated by particle transport modelling. This was accomplished by simulating cross-channel transport of particles between Mozambique and Madagascar, and between their shores and Europa Island, using an individual-based model (IBM) developed with Ichthyop 3.2 and driven by Regional Ocean Model System (ROMS) outputs of a South-West Indian Ocean Model (SWIM). Europa's octocoral species richness (33 species) was rather low for such a protected, relatively pristine environment within the region. Furthermore, while certain 'fugitive' alcyonacean species were noticeably abundant, other soft corals were rare or absent. The Europa soft coral community is thus possibly unique in its impoverishment within the Mozambique Channel, and the underlying reasons for this may be due to relative isolation of its reef communities, as suggested by the results of SWIM analyses. These revealed that the shortest transit times of particles in the Mozambican Channel were between northern Mozambique and north-west Madagascar (3 days), and between south-west Madagascar and Europa Island (4 days). These times are well within the competence period of alcyonacean larvae. Thus, while the north-west coast of Madagascar appears well-connected with the northern Mozambique coast, the most likely source of soft coral recruits at Europa Island would be the Tulear region further south in Madagascar, which also appears to have an impoverished soft coral fauna.

Keywords: larval dispersal, particle transport modelling, oceanographic eddies, East Africa, Madagascar

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Environmental drivers effects on the structure and functioning of rhodolith marine habitats in Central-Eastern Atlantic Islands

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The spatial configuration of rhodolith seabeds in oceanic islands provides an ideal system to assess whether environmental drivers regulate the structure and functioning of rhodolith seabeds across a depth gradient. Similar to altitude in terrestrial habitats, subtidal habitats experience abrupt environmental gradients (e.g. light, temperature, water motion, etc.) across narrow vertical (depth) scales. In this study, we characterized the structure of rhodolith habitats (size and shape of nodules) as well as their associated biota (fauna and flora communities) across depth scales in three Eastern Atlantic oceanic islands: Madeira (Portugal), Gran Canaria (Canary Islands, Spain), and Príncipe (Democratic Republic of São Tomé and Príncipe). A characterization program was performed in rhodolith beds at two sites and three different depths in the selected islands with subtropical waters (Gran Canaria and Madeira) and tropical waters (Príncipe). Samples were taken using SCUBA at each of the three depth strata. On each stratum, n=5 random replicates (25 x 25 cm) were taken each time, by collecting all rhodolithic nodules up to 5 cm deep. Rhodolith nodules were mainly larger at intermediate depths in Gran Canaria (25 m respect to 18 and 40 m) relative to the other depths; meanwhile sizes increased with depth in Madeira (16 m to 34 m) but decreased across bathymetrical gradient in Príncipe (5 and 10 m respect to 20 m). Most rhodoliths were quasi-spheroidal across depths in all studied islands. Still, the percentage of spheroidal rhodoliths was slightly lower at deeper strata, especially in Principe sites. The structure and functioning of the community assemblages changed consistently with bathymetry but overall with the additional substrate provided by the epiphytic associated biota (mainly macroalgae). Our data also suggested that different environmental drivers such as wave-induced turbulence (in upper layer) conditioned by geographical position of rhodolith beds in each island and irradiance attenuation (in the lower layer) can regulates the structure and functioning of rhodolith habitats across depth gradients in the studied islands.

Keywords: associated epibionts, calcareous algae, light penetration, vertical gradient, water motion

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What functional space to use to characterize species functions in ecosystems?

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Understanding processes leading to changes in biological communities require accessing functioning of ecosystems. Not all species within ecosystems fulfill the same role nor do they have the same sensitivity to environmental changes, therefore species function need to be quantified. However, characterizing species functions presents a challenge because it is time consuming and complex, even if we focus only on a single trait for a single species. Moreover, the overwhelming number of species present in tropical marine ecosystems, for example, make functional consideration almost prohibitive. Here we propose to use novel measurements to study functional variation in fish assemblages. Intuitively, tall people are naturally fitter than short people to play competitive basketball; this intuition takes root in the rules of biomechanics. Such rules can be used to understand what species can do in an ecosystem. We propose to use this approach to quantify functionality within tropical fish assemblages. To this end, we measured various anatomical features, such as mandible mechanical advantage (correlated to biting force), caudal fin shape (correlated to the type of locomotion), and eye focal-number (correlated to the quality of vision). These trait metrics were subsequently used to build a functional space, which is a sort of multidimensional map of fish functions in an ecosystem. Two other classical spaces were built: one based only on fish shape and another only on ecological information, which are common metrics used in literature. Simulated fish assemblages were constructed based on real coral reef data and were gradually degraded to highlight a fishing impact (ecosystem erosion) or coral mortality for example following bleaching (shift in ecosystems). Based on the three different functional space and these simulated assemblage functional metrics were calculated to test the detectability of changes based on methodological approach. Results showed that every space was useful to detect drastic ecosystem changes (species disappearance), but only biomechanics-based functional space allowed to accurately quantify subtle changes. Such result is encouraging to improve detectability and orientation in ecosystem changes but important work remain to be done to propose fish based indexes for health monitoring of reef ecosystems.

Keywords: functional space, fish assemblage, coral reef ecosystem, morphology, biomechanics

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Monitoring one of the world's largest breeding populations of frigatebirds

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Seabird colonies enrich shallow waters surrounding the islands they inhabit through the deposition of nutrient-rich guano, which in turn supports complex marine ecosystems. Frigatebirds rely almost exclusively on islands for breeding, and like other seabirds, they face a multitude of anthropogenic threats both on land and at sea, which have led to severe declines in some parts of their range. UNESCO World Heritage Site Aldabra Atoll is home to the largest breeding frigatebird colony in the Indian Ocean, if not the world. As a mixed colony of two species – greater and lesser frigatebirds – the combined breeding population is estimated to number at least 11,000 pairs. The sensitivity of Aldabra frigatebirds to disturbance, combined with their biennial breeding pattern, makes it difficult to accurately monitor their breeding population, and population surveys were inconsistent before 2010. However, due to its significance, annual trends in Aldabra's breeding population are now being monitored with an annual count of all active nests that was instigated in 2011. Since 2017, the breeding cycle of each species has also been closely monitored to document differences between the two species and to make comparisons with past surveys. Annual nest counts so far suggest that breeding populations of both species are stable and have not changed significantly the 1960s. However, breeding cycle monitoring shows that the timing of lesser frigatebird breeding differs markedly from greater frigatebirds and also to that recorded in the 1960s and 1970s. For both species, breeding cycle monitoring provides context to the annual nest counts, allowing better interpretation of the results. Given the importance of islands for frigatebirds, and of seabird colonies for coral reefs, continued monitoring of the major breeding colony on Aldabra, a fully protected atoll, could eventually provide an indication of the health of Aldabra's marine ecosystem and also of frigatebird populations in the Indian Ocean.

Keywords: Aldabra Atoll, breeding colony, conservation management, Fregata, seabird

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Population decline in key oceanic seabird colony of the Eastern Indian Ocean: Could illegal egg harvesting be the prime cause?

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We performed population counts of a nesting colony of terns (Sternidae) on Pitti Island, an official seabird sanctuary, on three different field occasions: 17 February 2013, 10 March 2013, and 10 February 2014. We also evaluated both seabird population trends using data from earlier surveys and the present survey. We assessed the number of nests as well as eggs. We also recorded egg loss due to predation, including collection and harvesting by fishermen. We conducted a questionnaire survey and interviewed 800 respondents from Kavaratti Island in the Lakshadweep Archipelago to assess the number of people involved in seabird egg harvesting and trade. We also evaluated their attitudes towards seabird conservation. Even though, we observed three tern species in the Pitti Island: Sooty Tern Onychoprion fuscatus, Brown Noddy Anous stolidus, and Greater Crested Tern Thalasseus bergii, we found only Sooty Terns nesting during our field visits. Natural predation on Sooty Terns is low ($< 1\%$), however, fishermen removed 14%–45% of the eggs. In our study, we found 72% of the 800 respondents were either directly or indirectly involved in the harvest including the egg trade. During our survey , we found Interviewees involved in egg collection and harvesting were significantly less inclined to support seabird conservation. Pitti Island is a protected area; nonetheless, tern numbers have been decreasing since 1963. Stringent conservation measures and periodic monitoring of the nesting colonies can only save this key pelagic seabird breeding site from being lost. Another important measure is to deviate the local people from the illegal egg collection and trade.

Keywords: seabird population decline, illegal egg harvesting, Pitti island, Eastern Indian Ocean, seabird colony, Sooty Terns

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Tracking tropical seabirds at sea: intra- and interspecific differences in the foraging ecology of white-tailed and red-tailed tropicbirds on Indian Ocean islands

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Tropicbirds are key pelagic seabirds in the Indian Ocean and breed on islands throughout the region. As top-marine predators, they are valuable indicators of ocean health, but their foraging ecology, and how they make use of ocean resources, remains poorly understood. This study aims to fill this gap in our knowledge of tropicbird biology by investigating the feeding ecology of the red-tailed and white-tailed tropicbirds *Phaethon rubricauda* and *Ph. lepturus*. More specifically, we determine the feeding distribution of birds using miniature GPS loggers, delve into their detailed at-sea behaviour by combining spatial data with depth and immersion loggers, and link these data with diet, using DNA metabarcoding techniques on faecal samples. To test whether feeding strategies vary between populations and marine environments, we compare two island populations of breeding white-tailed tropicbirds located in exploited and more pristine waters (Aride Island, inner Seychelles, and Aldabra Atoll, outer Seychelles, respectively). Finally, to evaluate how the two closely-related species avoid competition when breeding in sympatry, we compare the foraging strategies of red-tailed and white-tailed tropicbirds on Aldabra, one of the few places they coexist. We combine the latter with nest-based camera traps assessing potential differences in nest predation rates to identify the cause of recent red-tailed tropicbird declines and poor nesting success on Aldabra. Together, our findings provide the first complete picture of tropicbirds' foraging ecology during breeding, reveal differences between species and populations, address important ecological questions regarding competition avoidance between closely-related sympatric species, and provide important information for the conservation of tropicbirds and other seabirds breeding on Indian Ocean islands.

Keywords: foraging ecology, seabirds, competition, Seychelles, tropicbirds, biologging, movement ecology

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Unravelling the relative importance of top-down and bottom-up environmental effects driving vital rates according to sex, colony and experience in long lived species, the snow petrel

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Unprecedented climate change is expected to occur in the 21st century, with greater warming often reported for high latitudes. This should result in significant ecological impacts on ecosystems, from species to communities. Environmental factors and their ecological impacts on population dynamics need to be studied to understand the diversity of responses to climate change in living organisms. In our study, we used capture-recapture modelling based on a 36-year-long individual monitoring dataset to investigate bottom-up and top-down forcing on several demographic parameters according to the sex, the colony and the breeding status of individuals in a long-lived species, the snow petrel on Petrel island in Antarctica. Survival varied according to sex and previous state of breeding (reflecting the experience of birds). Experienced breeding males survive better than inexperienced non-breeding females. Predation and sea ice concentration had a greater negative impact on survival of inexperienced individuals. Breeding probability varied with the previous state of breeding, with a lower probability for inexperienced individuals, between colonies and previous breeding experience. Interannual variations of breeding probability for inexperienced breeders were partly explained by sea ice concentration during the pre-laying period. By contrast, sea ice concentration of the preceding summer had a positive impact on experienced birds. Hatching probability depended on colony, sex and previous state of breeding, and was negatively related to the southern annular mode and the number of snowy days during the incubation period. Air temperature and wind strength during the incubation period mainly affected non-breeders of the previous year. Fledging probability depended on colony and previous state of breeding, and its variations appeared to be better explained by local environmental factors. Breeding phenology partly explained variations in fledging probability. These results highlight the importance of top down and bottom up environmental factors on the demography of a long-lived species, and of taking into account multiple parameters to understand the demographic response to environmental fluctuations. We also emphasize the importance of local factors at the colony scale on demography, highlighting the need for multiple site studies to understand the impact of environmental changes on population dynamics.

Keywords: demography, sea ice, capture mark recapture, Antarctic, seabirds

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Exploring what movements matter in a critical eco-epidemiological situation, the case of avian cholera in seabirds of Amsterdam island

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Infectious diseases can be a threat for wild populations and the spatial ecology of these diseases need to be explored to understand how infectious agents circulate in spatially structured ecosystems such as islands. On Amsterdam Island (southern Indian Ocean), *Pasteurella multocida*, the bacteria responsible for avian cholera, causes recurrent mortality of albatross and penguin chicks. Different types of movements of individuals, from foraging to migration and prospecting, could play a major role in the circulation of the infectious agent at different scales. The main purpose of this study is to evaluate the potential role of different species in the dissemination of *P. multocida* with a combined study of movement ecology and eco-epidemiology. We considered potentially involved behavioral processes such as foraging movements of brown skuas (*Stercorarius antarcticus*) and within-season prospecting movements of Indian yellow-nosed albatrosses (*Thalassarche carteri*). We deployed UHF-GPS loggers on breeding skuas and non-breeding albatrosses during avian cholera outbreaks. We show that the skuas spent an important time in the colonies of albatrosses and in different places around the island, but did not hold feeding territories. In addition, we found very high seroprevalence and titers of antibodies against *P. multocida* among the sampled individuals, suggesting that they could play an important role in the circulation of the infectious agent. We also show that Indian yellow-nosed albatrosses in breeding failure or pre-breeding individuals can visit different conspecific colonies on the island, suggesting they could also play a role in the spread of *P. multocida* among breeding patches of this locally abundant but threatened species. Our study identifies various movements that may be involved in eco-epidemiological dynamics in multi-host/parasite systems and that their careful characterization is important for basic and applied reasons.

Keywords: habitat use, disease ecology, Pasteurella multocida, movement ecology, seabird

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Genetic diversity and colony isolation in one of the world's most endangered seabirds, the Mascarene petrel (*Pseudobulweria aterrima*), endemic to Reunion Island (Indian Ocean)

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Tropical petrels of the genus *Pseudobulweria* are among the least known and most endangered birds in the world. The Mascarene petrel (*Pseudobulweria aterrima*) is a very poorly known and critically endangered seabird endemic to Reunion Island. This species has an extremely small population estimation (100-200 mature individuals) suffering several anthropogenic threats as predation by introduced mammals and light pollution leading to stranding. Fifteen polymorphic microsatellites loci were isolated from this species in order to analyse genetic diversity, inbreeding and colony isolation, but also contemporary effective population size estimation and search for population bottlenecks. Analysis were done on individuals from two breeding colonies and on individuals found grounded as a consequence of light pollution. We found a surprisingly high level of genetic diversity and no significant deviation from Hardy-Weinberg Equilibrium, suggesting an absence of inbreeding. The analysis of genetic structure highlighted a slight but significant genetic differentiation between the two breeding colonies, suggesting high levels of natal philopatry and few exchanges between colonies. We also found that Mascarene petrel population probably has probably undergone a bottleneck. These results confirm that conservation actions engaged by the European Life+ Pétrels project since 2015 are strongly needed, and should be implemented independently for each colony to maintain genetic diversity.

Keywords: conservation, *Pseudobulweria aterrima*, microsatellites, genetic diversity, genetic structure.

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Connectivity within an oceanic seamount system: comparative phylogeography of widely-distributed benthic invertebrates from the Indo-West Pacific

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Analogous to oceanic islands, seamounts, which constitute one of the largest marine biomes on earth, offer a set of fragmented habitats in which benthic species with poor dispersive ability may undergo divergence in allopatry. This scenario have led many studies to interpret the originality of seamount-associated fauna as endemism resulting from the genetic isolation forced by the habitat fragmentation. However, the biogeography of seamount fauna remains poorly known, as less than 1% of the world's seamounts have been investigated. Moreover, many marine organisms have one or more highly dispersive phases in their life cycle (e.g. gametes, larvae and/or adults), which should hinder allopatric divergence among distant seamount populations. Based on samples from 16 deep-sea cruises carried out by the *Tropical Deep-Sea Benthos* research program across the Indo-West Pacific, we investigate the intra- and interspecific genetic divergence in 170 octocorals of the genus *Chrysogorgia* and 150 galatheids of the genus *Agononida.* These two taxonomic groups are characteristic of seamounts benthic fauna and share a common distribution range that encompasses two biogeographic barriers: the Indo-Malay archipelago separating the Indian and the Pacific oceans and the vast open ocean separating the Western and the Central Pacific. Using RAD-seq and based on four lanes of Illumina sequencing, we first use coalescent-based approaches to species delimitation using genome-wide SNP data and compare outputs with the primary species-hypotheses based on standard mitochondrial barcodes. Within delineated species, we then examine the connectivity patterns among seamounts and across the biogeographical barriers. Overall, our study enable the coupling of robust biodiversity assessment with investigations into species distribution and divergence processes in the deep-sea, which is of great interest with regard to the appraisal of seamount biodiversity, conservation efforts and global taxonomic initiatives.

Keywords: dispersion, fragmented habitats, genetic divergences, benthos, next generation sequencing

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[*] Speaker

Palaeo-biology / Palaeo-environments

Contents

Living on the edge: the effects of long-term climate change and fire activity on the remnant cool temperate rainforests of Tasmania (Australia)

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In a world where ecosystems are threatened by climate change, environmental disasters, and human disturbances, acquiring information about past environmental change and species responses is crucial to develop meaningful conservation plans. Wildfires are one of the major ecosystem disturbances worldwide and are projected to increase under the future climate change scenarios, especially in temperate regions. In this context, wildfires threaten the remnant patches of Gondwana-linked temperate forests of the island of Tasmania, Australia. A case in point are Tasmanian montane rainforests, which form at high elevation (ca. 700-1000 m a.s.l.) and are dominated by endemic tree species, such as the UNESCO heritage-listed trees *Athrotaxis cupressoides*, *A. selaginoides* and *Nothofagus gunnii.* These tree species display several life history attributes that suggest they are poorly adapted to disturbance by fire, including poor seed dispersal, slow growth to maturation and high stand mortality. Montane rainforest communities have suffered major fire-driven landscape-scale losses over the last 200 years and today cover less than 5% of the Tasmanian landscape. To date, these populations have not shown post-fire recovery and it is still unclear whether this loss of resilience is the result of 1) an insufficiently long fire return intervals or 2) climate change is now precluding the recovery of these species to fire disturbance. Here, we use species distribution modelling and palaeoecology to assess and test the influence of long-term climate change on the resilience to fire of the endangered temperate montane rainforests of Tasmania. Thanks to our long-term approach, we managed to distinguish high resilience locations, where montane rainforest was able to withstand past fire disturbance through a phase of dry climatic conditions. Our study indicates that climatic change between 3000 and 4000 cal yr BP drove a disequilibrium between montane rainforest and climate across much of the range of this vegetation type. Current and future climate change are likely to shift the climatic envelope of this plant community further, suggesting that current high resilience locations may face a reduction in resilience.

Keywords: resilience, montane rainforest, Tasmania, Australia, climate change

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Archipelagos in the Anthropocene - the legacies of past human-environment interactions on islands

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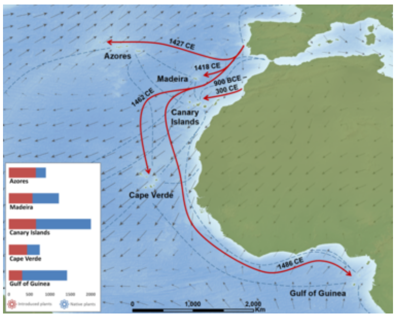

Human activities fundamentally alter ecosystems and landscapes from local to global scales. A key moment in making human impact truly global was the arrival of Columbus to the Americas in the late 15th century. The islands in the eastern Atlantic Ocean were crucial stepping-stones for this event and allowed for the subsequent emergence of global trade networks. These islands facilitated the biotic and cultural exchanges in the current epoch and as such, played a crucial role in the start of the Anthropocene. The aim of our study is to understand to what extent past human-environment interactions have shaped present-day landscapes and ecosystems on 30 islands in the eastern Atlantic. Volcanic oceanic islands are ideal "microcosms" for analysing the dynamics of past human impacts because the start of ecological processes and first human contact can be clearly defined. We integrate palaeo-ecological- and historical socioeconomic data spanning the duration of human settlement with a GIS-based analysis of anthropogenic, climatic and topographic variables. As a proxy for the state of island ecosystems and landscapes, we quantified the proportion of natural vegetation and calculated an index for the degree of landscape modification. Our findings show that present-day ecosystems and landscapes are the outcome of how humans have interacted with their environment over several centuries and sometimes millennia. However, contrasting pathways of past human-environment interactions result in diverse ecological and landscape outcomes. We conclude that an appreciation of the dynamics of local human-landscape interactions in the past provides a reference point for understanding current global change.

Keywords: Atlantic islands, ecological systems, environmental history, human activities, social, topography

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[*] Speaker

A new record of human settlement and past environmental change of the Comoros

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As humans have colonized new places, they often initiate dramatic environmental change, even in the distant past. On remote islands, where levels of endemism are high, species and environments are often particularly vulnerable to the effects of introduced species like humans, and the plants and animals they deliberately or accidentally bring with them. The first study of the environmental history of the Comoros, a volcanic archipelago in the far western Indian Ocean, was conducted in 2016 in order to test the hypothesis that the Comoros were stepping stones for prehistoric human migration from east Africa to Madagascar. Sediment cores collected from the island of Anjouan along an altitudinal transect incorporated a range of ecologies including lowland swamp gardens (Ntrontroni Swamp - 10masl), upland dry forest (Dzialoutsounga Crater - 710masl) and upland wet forest (Lake Dzialandze - 925masl). Preliminary results from Ntrontroni Swamp show that a shift from a swamp forest and and a lagoonal system to a peat swamp occurs around 1000 years ago soon after deforestation. Pollen and phytoliths identifying taro, cotton, rice and various spice trees (nutmeg, cloves) reveal the introduction of agricultural crops to the island as early as AD 900, with rice appearing around AD 1400. In addition, analysis is underway for all sites including ITRAX, humification, pollen, charcoal, and phytolith analysis and this will be reported on in this paper. This research will contribute to our understanding of patterns and chronologies of human colonisation, as well as the environmental impacts that humans have had. The pollen and charcoal records show dramatic changes in vegetation and fire regimes in the last 1500 years that are best explained through the influence of human settlement. Such studies of the past are extremely useful for better understanding and mitigating the effects of human-induced environmental change today.

Keywords: pollen, charcoal, palaeoecology, human migration, Comoros

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*Speaker

When were the Azorean Islands really colonized? A high-resolution paleolimnological approach

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The discovery and colonization of islands are crucial to understand the colonization patterns of new territories, the spread of languages, past economic trade, diffusion of past societal and knowledge during the past millennium. However, historical and archaeological records are scarce and incomplete on many islands, including the Azores, hampering the determination of the exact age of first human settlements. The most commonly accepted date for the first settlement on the Azores islands based on historic documents is 1432 A.D. However, a recent environmental reconstruction of São Miguel island that covers the last 730 years clearly shows that the first-settlements of this island took place by ca. 1287 A.D., approximately 150 years prior to the currently recognized colonization. Here we present a new perspective, using both classical (e.g. pollen and spores from higher plants, fungal spores, algae remains, charcoal particles, plant and animal fragments) as well as cutting-edge approaches (e.g. ancient DNA and faecal related organic compounds) to unequivocally trace the first signs of human activity preserved in long continuous sequences of natural sedimentary archives. Our objective was to perform robust high-resolution climate and environmental reconstructions for the last millennium in order to pinpoint the date that the first settlers arrived, the timing of island occupation and the spread of new settlements. These reconstructions were performed using a multiproxy characterization of sedimentary lacustrine records located on five islands distributed in an NW-SE transect. Preliminary data constrains stratigraphic points that characterize two phases of occupation of Azorean Islands. First human activities started on several islands with the introduction of cattle, extractive forestry and cereal cultivation, followed by extensive deforestation and the large-scale introduction of exotic species on land and into lakes (e.g. exotic plant species and fish introductions), which shaped the present-day lake ecosystems.

Keywords: Paleolimnology, Azores, classical and cutting, edge approaches, colonization patterns, climate and environmental reconstructions

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*Speaker

Biodiversity dynamics after human arrival on islands: are islands at an ecological crossroad?

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Human activities are increasingly dominating ecological systems and are often considered the main drivers for ecosystems change. The need to quantity the speed of human impacts in ecosystem dynamics have caused a controversial debate on natural baselines and the start of the Anthropocene. However, it is now increasingly evident that hardly any "natural" baselines are available for timescales with sufficient available data (e.g. thousands of years). Oceanic islands are rare exceptions, many of which have been sheltered from human impacts due to their isolation from the continent. Oceanic islands thus provide repeated, complex systems with an excellent opportunity to quantify the direct effect of human impacts after their arrival on the islands (pre-human baseline) on the local vegetation. Here, we tackle this challenge using palaeoecological datasets of fossil pollen time-series covering the past 5000 years. We gathered these datasets from Neotoma database and other published sources. We selected oceanic islands that together covered large gradients of: latitude, elevation, size, distance from continent, and human arrival times. We calculated a "system state metric" using the pollen time series and a combination of Bray Curtis similarity analysis and ordination analysis (NMDS). We also applied a breaking point analysis to calculate whether the vegetation composition changed abruptly or otherwise followed a constant transformation over time. Preliminary results, showed that in many islands there is a vegetational compositional change that seems to start around human arrivals. However, we found that in other islands major vegetation changes may happen without human presence on the island. These independent records on multiple island ecosystems will inform a novel model framework to simultaneously quantify ecosystem dynamics and structure prior to human arrival (and its associated impacts), and also those that occurred after human arrival; this will allow identifying the main changes that humans have caused in island ecosystem processes.

Keywords: Holocene, Oceanic Islands, Palaeoecology, pollen records

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*Speaker

Tracking human impact on island ecosystems by detecting ”ghost taxa” with ancient DNA

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Islands ecosystems have been transformed since the early stages of human settlement. Loss of natural vegetation, and in particular forest cover, is one of the main consequences of human colonization. However, it is difficult to assess the rate of such deforestation processes, especially on islands that have a long history of human occupation. Understanding the transformative processes that island ecosystems have experienced is essential for their effective management and preservation today. The analysis of palaeoecological records and fossil indicators provides the long-term perspective needed to study these processes, while delivering different ecosystem baselines to be used by managers as references for restoration and conservation actions. Within Macaronesia, the Canary Islands were the earliest islands to be colonized by humans (at least 2000 years ago) and the only islands to undergo a double colonization (aborigines and Europeans). However, the precise timing and extent of human impacts on Canarian ecosystems are poorly known, and consequently restoration and conservation management targets usually fail to incorporate pre-human ecosystems. In addition, palaeoenvironmental reconstructions can be limited due to poor conditions for fossil preservation at certain sites, i.e. ”*silent sites*”, and under-representation of several key taxa in the fossil record, i.e. ”*ghost taxa*”. Althought there is evidence for human induced changes in forest composition, under-representation of certain key taxa such as Lauraceae (the dominant trees in the Canarian evergreen laurel forest) prevent us from determining the true forest composition or confirming the former distribution of forest types at local or regional scale. Combining the analysis of palaeoenvironmental DNA (PalEnDNA), i.e. ancient DNA from disseminated genetic material, and traditional palaeoecological proxies, we aim to improve the detection of such ”*ghost taxa*”, but also increase the taxonomic resolution to obtain better reconstructions of past Canarian forests. For the first time we isolate PalEnDNA from Canary Island sedimentary deposits at forest sites. Detection of Lauraceae PalEnDNA within the sedimentary sequences indicates when these trees have been components of the forest and show how PalEnDNA can be an effective tool in the identification of ”*ghost taxa*” from palaeoecological records on similar island environments.

Keywords: ancient DNA, Canary Islands, laurel forest, palaeoecology, past vegetation

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Archaeobiogeography of extinct rice rats (Oryzomyini) in the Lesser Antilles during the Ceramic Age (500 BC to 1500 AD)

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In the Lesser Antilles, rice rats (Oryzomyini tribe) – now extinct in the region – were one of the few non-flying terrestrial mammals to be present and eaten by the pre-Columbian ceramic societies inhabitants (between 500 BC to 1500 AD), before the arrival of European settlers. Rice rats have a dual interest, both biological and cultural. As extinct taxa, their morphologies, as well as their past distribution and diversity in the region are poorly known, yet they allow to study the diet of pre-Columbian humans. We aim to characterize the spatiotemporal distribution of rice rats, complete their systematics and taxonomy, and assess their relationship with humans. We used an integrative approach combining geometric morphometrics, genetics and zooarchaeology. Using a two-dimensional sliding semi-landmark based geometric morphometric approach, we quantified and visualized tooth size and shape differences between chronological cultural periods and between islands. To test whether the phenotypic groups reflect environmental adaptations or phylogenetic history, we conducted ancient DNA analysis on the mitochondrial genome (Cytochrome b gene) of 70 archaeological specimens originating from all studied islands. From the 659 archaeological specimens representing seven different islands of the Lesser Antillean archipelago, three morphological groups emerged. They were geographically consistent and present from the beginning of the Ceramic Age: one in Saint-Martin in the northern part of the archipelago characterized by very small molars, one in Martinique in the south, and one in the central region (*i.e.* Antigua, Barbuda and the Guadeloupe archipelago: Basse-Terre, Grande-Terre and Marie-Galante). Within the central region each island has its own morphotype. Our morphometrics data reveal a archaeobiogeographic signal defined by a clear pattern of past distribution of Oryzomyines in the archipelago, stable over time. It suggests a limited human influence on the spatiotemporal distribution of this rodent. The wet and hot environmental condition typical of the tropical regions do not favor DNA preservation and likely preclude DNA analysis of the ancient remains we have studied so far. Yet, the phenotypic geographic distribution appeared consistent with DNA clusters from previous studies and indicates that new taxonomic classifications should be designated for the extinct archaeological populations of Saint-Martin and Marie-Galante.

Keywords: geometric morphometrics, genetics, teeth, Rodents, island evolution

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*Speaker

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Cylindraspis - from whence thou hast com'st to thine home? Mitogenomes give the answer

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Cylindraspis is a genus of extinct giant tortoises endemic to the Mascarene Islands. Recently it has been suggested that humans have introduced these tortoises, spurring a debate about their origin. To contribute further insights into this matter, we produced almost complete mitogenomes for all five currently recognized species. We applied optimized NGS protocols for ancient DNA approaches, including single-stranded library preparation, and in-solution hybridization capture. We included the resulting data in phylogenetic, molecular clock, and biogeographic analyses using mitogenomes of representatives of all extant genera and species groups of tortoises (Testudinidae) with all extant taxa from Madagascar and the Seychelles represented. The mitogenomes of all five *Cylindraspis* species were deeply divergent from those of any other extant tortoise. In phylogenetic analyses of the mitogenomes, all *Cylindraspis* species are monophyletic and sister to a clade containing tortoise taxa from Africa, Asia, Madagascar, the Seychelles, and South America. The divergence date inferred for *Cylindraspis* exceeds by far the age of the Mascarene Islands, while the divergence dates for the mitogenomes of two species pairs (*C. indica* vs *C. inepta* and *C. peltastes* vs *C. vosmaeri*) suggest dispersal and vicariance within the Mascarenes, explaining also the former occurrence of two sympatric species on Mauritius and Rodrigues. Biogeographic analyses including our complete data set suggest that the ancestor of *Cylindraspis* lived in Africa and arrived on the Mascarenes circumventing Madagascar. According to our data, the Mascarene giant tortoises were definitely not introduced by humans.

Keywords: ancient DNA, biogeography, Cylindraspis, giant tortoise, Mascarenes

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*Speaker

Combining species distribution models with dispersal kernels to predict range shifts in wind-dispersed organisms under changing climate conditions

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Species distribution models have been the most widely used tool to assess the impact of climate change on biodiversity patterns. One of the main assumptions of these models is that species are at equilibrium with their environment, as if they had no dispersal limitations. We test this hypothesis in spore-producing plants, wherein experimental evidence suggests that efficient short-distance dispersal coupled with random long-distance dispersal leads to an inverse isolation effect. Under the latter, a higher genetic diversity of colonizing propagules is expected with increasing isolation, counteracting differentiation beyond the range of short-distance dispersal. We employ spatial genetic structure analyses to show that the inverse isolation effect is not a rule in spore dispersal and that geographic distance remains a significant proxy of spore colonization rates, even in organisms with efficient dispersal capacities. We therefore present an integrative model to make predictions of range shifts in wind-dispersed organisms under changing environmental conditions, taking the spatial variation of species dispersal capacities into account. We combined species intrinsic biomechanical features (i.e., the settling velocity of diaspores and their release height) and environmental variables (i.e., canopy height, wind intensity and turbulence) into a mechanistic analytical long-distance dispersal model. We then implemented this dispersal model using a new version of MigClim's cellular automaton that allows migration simulations of species across the landscape under competing environmental change scenarios. The new version of MigClim was adapted for wind dispersal by implementing spatially-explicit dispersal kernels taking variation in wind conditions and canopy structure across the landscape into account. We show an example of application of this method to predict how climate changes will impact future distribution ranges in bryophytes, which are particularly sensitive to climatic variations due to their poïkilohydric condition.

Keywords: dispersal ecology, dispersal kernel, climate change, spores

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[*] Speaker

Restoration Ecology / Ecological Restoration

Contents

Moving toward data-driven ecological restoration of vegetation in the Hawaiian islands

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Habitat loss and invasive species have drastically modified Hawaiian ecosystems. Numerous ecological restoration efforts seek to expand native dominated vegetation and provide habitat for endangered species. However many of these efforts are limited by incomplete information about baseline conditions or realistic objectives for endangered species. Mounting data now permits a more objective approach toward representing appropriate population densities of dominant and rare plant species in a spatial context. First, an extensive collection of vegetation plot data from over 1400 locations across all of the main islands provides a quantitative basis for assessing canopy cover in a wide range of climatic environments. A focus on high quality habitat necessitates considering only of vegetation plots with minimal invasive species cover and without a history of degradation from cattle grazing. Second, a comprehensive set of habitat suitability models, compiled in GIS and based on a wide range of source data, provides a spatial context for evaluating potential habitat. For a baseline set of 176 woody species with sufficient data, we assessed vegetation plots falling within each species' habitat envelope to determine its canopy cover under high quality habitat conditions. For these baseline species, we used ecological traits (dispersal mode, pollination mode, breeding system) and phylogenetic traits (whether it belongs to a monotypic, small or large colonist lineage) to build a multivariate model, which estimates the potential local abundance as measured by canopy cover. Species exhibiting wind pollination or a dioecious breeding system, or belonging to monotypic or small colonist lineages exhibited greater cover than species without those traits. This model was then used to estimate potential local canopy cover for the remaining species with insufficient data from vegetation plots. We then converted estimated canopy cover values to local densities (based on plant size) to provide a target density for out-planting of rare species. Combined with using habitat envelopes (among other criteria) to identify suitable reintroduction sites, these estimated densities represent a data-driven technique for rebuilding populations that have fallen due to severe anthropogenic alteration.

Keywords: Hawaii, restoration, vegetation

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Invasion impacts and medium-term benefits of controlling invasive alien plants in one the most invaded island forests worldwide

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High oceanic islands are often hotspots of endemic species subjected to strong and rapid anthropogenic impacts that lead to high extinction and endangerment rates of their biota. Mauritius, an oceanic island in the Indian Ocean champions the highest levels of extinction per land area in the world, and similarly, extreme levels of invasion by alien species. To better understand impacts of alien plants and lost of potential frugivores on native plants, we monitored temporal changes in woody native plants in permanent plots of 0.01 and 1 hectare located in one of the island's best preserved wet forest remnants. We sampled 28,000 woody plants reaching at least 1.3 m high in forests cleared of alien plants at least five years previously to compare with nearby control areas (non-weeded forests). Plants were permanently tagged, identified to species level and their stem diameter measured. In non-weeded plots, the number of individuals, biomass and species richness of native woody plants steadily decreased through time (5 to 15 years), with recruitment of new native individuals being virtually nil, whereas in weeded areas the opposite was observed. Recruitment in managed areas were mainly of lianas, understory and fleshy fruited species. Timely weeding also averted imminent plant species extinction. To halt and reverse the on-going degradation of protected forest remnants in Mauritius, control of alien plant species must be considered the utmost priority. Management actions like thinning of native species or planting within areas with a matrix of good quality remnants should be strongly discouraged as they bring no tangible results apart from slowing down restoration progress. At the scale of our study, extinction of the largest birds and reptiles apparently do not have much of a negative effect on the vast majority of native fleshy fruited species which appear to regenerate well shortly after alien plants are controlled. However, the recent mass-culling of the Endangered Mauritius flying fox, the last animal species able to handle large seeded species, might have profound negative effects as at least 53% of native woody plants of the wet forests have their fruits eaten by this native frugivore.

Keywords: conservation management, ecological restoration, forest, invasive alien plants, plant animal interaction

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*Speaker

Ecological processes shaping community dynamics in seasonally dry tropical forests: lessons learned from a restoration program on Réunion island

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Understanding how ecological processes control community asssembly during secondary succession remains one of the greatest challenge in ecology. In a global context of habitat degradation and climate change, restoration ecology provides opportunities to both test ecological theories and optimize restoration actions. Although well documented in tropical wet forests, the importance of environmental filtering and biotic interactions in community assembly are less known in seasonally dry tropical forests (SDTF), yet among the most threatened ecosystems worldwide, particularly on densely populated islands. Here, we study the population dynamics of early life-stages trees in a restoration program of SDTF on Réunion island that includes afforestating 9 ha of secondary savannah. We specifically aim at understanding the effects of abiotic filters, in relation with climatic constraints, and biotic processes such as competition and facilitation on individual performance. We investigate the survival and growth of 6292 individuals in 45 species between 2012 and 2017 in various conditions of planting density. In each survey plot, abiotic descriptors, such as slope, elevation and rainfall, were recorded. Species composition and intra-plot cover were monitored between 2012 and 2017. Our results show that environmental changes during the first year after planting have a strong impact on the survival of seedlings and on their relative growth. In particular, rainfall amount, especially during the dry season, act as a major determinant of seedlings survival, shifting species composition in plots. Globally, fast-growing species experiment a higher mortality than slow-growing species at all censuses. Although stems density seems to positively impact mortality through time, shadowing provided by fast-growing species increase overall survival even at early-stages. Those results highlight how restoration can improve, not only future restoration works, but also theories in community ecology. As expected, environmental filtering, especially water-availibilty, drive communities dynamic in SDTF. Furthermore, early intra-community effects of competition and facilitation appeared to act as strongly on species survival and growth. At local and regional scale, this study provides tools for SDTF restoration to potentially optimize survival, growth and eventually the assembly of native plant communities.

Keywords: restoration, dry forests, community dynamics, environmental filtering, biotic interactions

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Rewinding for rewilding: Suppressing the brown tree snake to reintroduce the endangered Guam kingfisher

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Plans to reintroduce the Guam kingfisher *Todiramphus cinnamominus* (Family Alcedinidae; Chamorro: Sihek) to its native range are under development. Historically limited to Guam in the western Pacific Ocean, the kingfisher was listed as endangered in 1984 and declared extinct in the wild in 1988. Its current population of about 140 individuals has been maintained by captive breeding on the mainland United States and Guam, beginning with 29 birds collected in 1984 and 1986. The invasive brown tree snake *Boiga irregularis* (Family Colubridae), native to parts of Australia, Indonesia, and Melanesia, is credited as the main driver of native wildlife species loss on Guam. With no known means to eradicate the snake, methods to suppress the brown tree snake population are being tested. One such method involves delivery by helicopter of dead neonatal mice bait laced with a toxicant that kills snakes, acetaminophen. Mice attached to small parachutes are deployed into treetops where snakes forage; treetop deployment also limits impacts to vulnerable non-target species on the forest floor. The hope is to reduce the snake population below a threshold that allows coexistence with native wildlife. There are possible confounding factors, so lessons learned from other native species reintroductions and other invasive species management programs will inform success of a future Guam kingfisher reintroduction. For instance, survival of reintroduced kingfishers might also hinge on mitigating other risks likely associated with the kingfisher extirpation in the first place and that are common threats to native species on islands, e.g., habitat degradation and other invasive species, such as rats and feral cats. Additionally, recent cases of new invasions following eradications, e.g., when mice become invasive subsequent to rat eradications, must be considered; we should anticipate surprising outcomes. Newly established invasive species can be transformative, as can reductions in populations of established invasive species responsible for generating transformative impacts. Will rewinding an impact recreate conditions favorable for reestablishing the kingfisher?

Keywords: brown tree snake, endangered species, Guam kingfisher, invasive species, rewilding

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*Speaker

World's first successful national eradication of ring-necked parakeets Psittacula krameri

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There have been relatively few successful eradications of invasive alien birds compared to eradications of invasive mammals. The ring-necked parakeet (*Psittacula krameri*) is the most widely introduced parrot species on the planet, having been introduced to more than 40 countries across five continents. Control and management of the species is common but, until this year, the species had not been eradicated from any of them. In the Seychelles, ring-necked parakeets were introduced as pets from the 1970s and accidentally released birds established a small breeding population on the main island of Mahé by the late 1990s. The rapidly expanding parakeet population caused increasing damage to agricultural crops and, as a high-risk reservoir host and vector for pathogens, including beak and feather disease virus (BFDV), the population posed a major threat to the endemic Seychelles black parrot (*Coracopsis barklyi*), which occurs only on the nearby island of Praslin. An eradication programme to remove ring-necked parakeets from Seychelles started in 2012 by the Seychelles Islands Foundation. We present the eradication methods tested and applied and the results of the control efforts in the three main phases of the programme; (1) monitoring of numbers and methods trials; (2) intensive elimination of ring-necked parakeets; and (3) post-eradication monitoring for verification of success. We also present the techniques of the nation-wide public information campaign which was a fundamental component of the eradication in all phases. A total of 548 birds were culled over 5 years, 95% with shooting and 5% with mist-netting. The most effective way to reach the general public was by the eradication team members going out and talking directly to people. The eradication was declared successful in early 2019, making Seychelles the first country in the world to officially eradicate an established population of ring-necked parakeets from the wild. Lessons learned from this eradication will prove valuable for eradication attempts elsewhere and this success should encourage such attempts, especially on islands.

Keywords: invasive alien bird, island, parrot, successful eradication, Seychelles

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Coral reef regeneration experiment with mineral accretion technology: a case study on Fregate Island, Seychelles

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Coral reefs, including those in the Seychelles, have been damaged through overfishing, dredging, pollution but also by frequent coral bleaching events. The bleaching of 1998 resulted in 98% coral mortality within the granitic Seychelles islands. There are extensive coral restoration projects in the Seychelles, which have generally focussed in increasing coral recruitment on destroyed reefs through coral nurseries and coral fragment transplantation. However, there is limited literature evaluating the success of such projects, despite the fact that such evaluations would greatly help the development of best-practise guidelines. We report the preliminary results of a novel, large scale experimental restoration study, in which 800 storm-derived coral fragments (corals of opportunity) were transplanted onto eight artificial structures situated at depths between 5 and 7m. In this study, the first of its kind in the Western Indian Ocean, we compared the growth rates of coral fragments growing with or without mineral accretion technology (MAT). MAT involves the electrochemical deposition of calcium carbonate (CaCO3) by electrolysis on three dimensional iron structures to improve growth rates of transplanted coral fragments. Transplanted coral fragments were subject to either 10A 20V direct current (4 MAT treatment structures) or no current (4 control structures). First year results indicate absolute growth and settlement rates on MAT structures were higher than coral fragments in the control treatment. Survival rates on both MAT and control were 85-90%, with *Acropora spp* and *Pocillopora spp* performing particularly well on both structures but grow faster on MAT. Our results demonstrate that mineral accretion technology promotes faster growth of coral fragments. As MAT can be readily be scaled up to cover large areas, these results suggest that MAT can thereby reduce the need to harvest coral fragments from healthy colonies, and increase the speed at which new reef habitat can be established to support fish and arthropod species.

Keywords: coral, restoration, rehabilitation, ecosystem function, seychelles

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Restoring degraded water catchments using ecosystem-based adaptation tools for long-term benefits of downstream communities in Seychelles

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The main threat to biodiversity on Praslin is forest fires which are aggravated during the long drought periods exacerbated by climate change. 40% of Praslin (1500ha) are affected by forest fires. Forests play a vital role in the protection of the island's water supply.The degradation of forests to contribute to droughts, and reduced river flows. To reverse the impacts, it is vital to restore the water catchments using natural solutions to ecosystem-based approaches. The research consists in rehabilitating degraded ecosystems (25 ha) to return them to a forest formation to restore ecosystem services such as healthy water catchment. The project focused on the two largest water catchments on Praslin: Fond Boffay (150 ha) and Nouvelle Decouverte (341 ha).The management approach developed focused on replanting non-native shrublands, which involved nursery-based propagation of native plants; land preparation consisting of cutting "strips"within shrublands (strip clearing) and planting these strips with native species; post-planting maintenance, data collection and reporting. New rehabilitation trials were set up to further develop knowledge on best rehabilitation practices and methods for the degraded lands of Praslin. 5.1 ha was rehabilitated during Phase 1. Rehabilitation is mostly limited by strip clearing of the land prior to planting. Considering practical constraints (workforce) and planting seasons, the maximum coverage achievable per year is ca. 5 ha. Planting density achievable is 400-500 plantings/ha, up to 1000 plantings/ha. Addition of charcoal and top soil results in more than double growth rate for plantings done on bare soil lands. Medium-term monitoring is required todetect differences in relative success between species or planting treatments. Based on previous trials, *Planchonella obovata* appears to be the most successful species. Other promising species that are are *Dodonaea viscosa*, *Ludia mauritiana*, *Intsia biguga* and *Mimusops sechellarum*. The rehabilitation work resulted in the development of key knowledge for better planning of future rehabilitation work on highly degraded lands. Although still modest (5 ha), it represents the largest rehabilitation work on highly degraded lands done since the late 20th century.

Keywords: Restoration, ecosystem, based adaptation, degraded forest, water catchment, climate change

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Strategic rewilding to restore seed dispersal to a defaunated island

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ecent declines, extinctions, and range contractions of vertebrates have disrupted important ecological functions, particularly on island systems. Restoration of ecological function requires rewilding of key species, often in the face of ongoing stressors, within heterogeneous and fragmented landscapes. As a result, successfully restoring ecological function is difficult, but islands provide an opportunity to develop strategies for restoration, which may then be applied across larger areas. Here, we assess the effect of frugivore loss as a result of the invasive brown treesnake (*Boiga irregularis*) on the island of Guam and develop a strategy for rewilding the island given the continuing presence of the snake. To determine how frugivores affect forest composition and structure, we compared Guam to nearby islands with vertebrate seed dispersers, using surveys, manipulative experiments, and a forest model. We demonstrate that Guam's forests will become less diverse and less able to recover from disturbance without vertebrate seed dispersers. We then developed a strategy to restore seed dispersal to Guam's forests. First, we assessed the seed dispersal effectiveness of 5 native birds, the Mariana Fruit Bat (*Pteropus mariannus*), and two non-native mammals currently present on Guam - the feral pig (*Sus scrofa*) and black rat (*Rattus rattus*). The native avian frugivores varied dramatically in their effectiveness, but the two bird species that had the broadest diets, positive impact on germination, and extensive movement across habitat types were selected as preferred candidates for reintroduction. While the non-native pig effectively dispersed seeds, the non-native rat did not; the pig may be a useful disperser in the short-term in particular habitats where it has fewer negative impacts. We then used a spatially-explicit model to identify the highest priority areas for rewilding the three frugivore species to restore ecological function, and the associated costs of invasive species control. Restoration of vertebrate seed dispersers in the presence of invasive predators may be an achievable goal on Guam, and could serve as a guide for rewilding efforts in other places that are under threat.

Keywords: rewilding, seed dispersal, restoration, ecological function, mutualism, invasive species

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Social Sciences on Islands

Contents

Global law as an analysing tool of climate change adaptation: what relevance for justice assessment of coastal governance?

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1

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This study aims to present "global law" theories and their usefulness, to highlight the role that law and lawyers may play for Islands governance to be adapted to global changes. Indeed, the hypothesis tested is that global law allows to consider the - otherwise invisible - actors *de facto* implicated in the rule-making and implementation processes at different levels, from local to global, but also the *continuum* between "soft" (or non-binding) and "hard" (or enforceable) law. In order to do so, the study mobilizes and defines some recent notions, derived from the ecological thinking applied to the law. For example, from a legal analysis perspective, the notion of " regimes complex " is helpful in order to designate the set of norms, actors and processes involved in islands governance, without being limited in our study by restrictive legal concepts, such as the judicial order, the formal legal value of the norms, or the *de jure* legitimacy of the actors considered. It permits to include in the study a sociological reading of a set of norms, to understand the circulation of these norms and to characterize them according to the actors who carry them. Adopting the situated point of view that global law recommends, reveals and, thus, may favour the process framing the interactions between various levels, *fora* and actors of law-making and law-implementation. Indeed, mapping applicable law to a given area or subject matter, like islands governance, actually depends from the point of view of the person answering the question, and the normative project he or she carries. This study main outcome is that global law helps to reveal the "relative" but also "dynamic" characters of the law that may frame island governance. Therefore, it allows to assess the existing normative offer, by referring to the sociological framework of justice, to identify accountability gaps of *de facto* powerful actors, and, more fundamentally, to focus attention on "connecting needs" to link for instance the issues of coastal governance and adaptation to climate change, or more broadly the issues of environmental and social justice.

Keywords: law, environmental justice, social justice, coastal governance, adaptation to climate change

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Addressing the research-management implementation gap at two UNESCO sites in the Seychelles

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There is a much-debated 'implementation gap' concerning the application of science to conservation management. The Seychelles Islands Foundation, a public trust which manages the UNESCO World Heritage sites of the Seychelles, provides a strong working example of the diverse ways that researchers and practitioners can work together to change island conservation strategy and policy based on scientific evidence. The sites, Aldabra Atoll, a remote and relatively undisturbed raised atoll in southern Seychelles and the Vallée de Mai, a palm forest on the island of Praslin, differ ecologically and in the conservation challenges they present, but similar evidence-based management strategies are applied at both. Long-term biodiversity monitoring is geared towards assessing trends in their objectively-assessed values, and threats to these values, including (1) population status of endangered/endemic iconic species such as the coco de mer and giant tortoise; (2) distribution and abundance of broader taxa or guilds, such as landbirds, herpetofauna and predatory fish communities; (3) ecosystem-level processes, such as plant phenology, avian breeding success and coral recruitment; and (4) threat status, such as invasive species alien presence and distribution. Most analysis of trends is done internally, and research collaborations are established with experts to resolve complex questions that address conservation needs and require specialised knowledge, such as genetic analysis or advanced statistics. Specific research agreements ensure productive collaboration benefitting all partners, with co-authored papers being the main outputs. The findings and recommendations feed back into site management, facilitating the process of adaptive management. Examples of recent research impacts and management responses at these sites include: (1) substantially extended protected area coverage; (2) amended visitor regulations and policies; (3) informed decisions on invasive species eradications; (4) implementation of a sustainable coco de mer harvesting scheme; (5) zonation of protected area and tightened fishing regulations; (6) regular review and modifications of monitoring methods; and (7) identification of future research priorities. There is room for improvement in the current system, but it largely ensures that monitoring data are analysed, relevant, and incorporated into management. We show that bridging the implementation gap can work in practice when institutional structures and resources are in place.

Keywords: adaptive management, evidence, based conservation, island conservation strategy and policy, biodiversity monitoring, knowledge, action boundary

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*Speaker

An approach to assess the socio-economic impact of conservation projects

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Small oceanic islands host unique ecosystems with important rates of flora and fauna endemism. But their ecosystems are also typically threatened by invasive species pressure and human settlement. Conservation projects have ecological and scientific impacts, but as they channel funds to, usually, rural areas they are also positive funding sources to the local economies. Based on the experience of the Safe Islands for Seabirds LIFE project, a methodology to assess the socio-economic impact of a nature conservation project on the local community is presented. The study focuses on the wealth created and the jobs supported directly and indirectly by the project. To assess the impact of the Safe Islands for Seabirds project (Azores, 2009-2012) a combination of methods to analyse the project expenditure, the jobs created directly as a result of it, and, by means of multipliers, the incomes and jobs it supported indirectly was used. During 2009–2012 period a direct expenditure of EUR 344,212.50 from the project increased the gross domestic product of the Azorean region by EUR 206,527.50. In addition to the 4.5 jobs created directly by the project, it also supported indirectly the equivalent of 1.5–2.5 full-time jobs. The project also provided the opportunity to preserve and promote natural amenities important for the quality of life of the local community. Findings show that a nature conservation project can have positive economic impacts, and recommendation is made to the creation of a standardized tool to calculate in a straightforward but accurate manner the socio-economic impacts of conservation projects. Conservation projects make sense on small islands due to their ecological characteristics, but they are also the opportunity to support these isolated and rural economies.

Keywords: conservation project, LIFE, multiplier, protected area, Corvo Island, socioeconomic impact

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*Speaker

Breaking the ”Poor data poor decision” loop. Strategies to balance geographic data- knowledge biases in marine spatial planning

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Management of human activities in the marine environment is vital for sustaining the health and function of marine ecosystems. Ecosystem-based management implanted through marine spatial planning (MSP) would ideally allocate human activity in a sustainable perspective. However, data and knowledge on marine environments and human uses at sea often suffer from shortfalls that cause great uncertainty regarding the current and future interactions between marine ecosystems and socioeconomic activities. At the heart of this uncertainty is the data abundance bias between more accessible and emblematic ecosystems and therefore more studied areas versus other areas. These shortfalls are illustrated along the 215 km coast of Reunion Island (Western Indian Ocean) between the well-documented coral reef coasts versus the rocky windward side. We examine the underlying social and technical driving factor to those data gaps and biases. Primary results reveal how the lack of biological and environmental data strongly drive management priorities and produce socio-environmental inequities through a ”Poor data poor decision” loop. We propose solution pathways to address these biases in MSP from the early stage of data collection to the advanced stage of proposing spatial management plan. We advise to apply MSP concepts to the zoning of future scientific investigation efforts in the marine geographic space. This study contributes to further development of the theory and practice of addressing data gaps, biases and uncertainty in MSP, especially in distant and/or deep waters compared to coastal waters.

Keywords: Marine spatial planning, marine conservation, ecosystem, based management, data shortfalls.

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*Speaker

Legitimacy of the scientific expertise and its media coverage in an island context: analysis of media corpus on the theme of shark risk in La Réunion

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Since 2011, fatal shark attacks occurred in Reunion Island and led to the "shark crisis", raising up different issues for humanities and social sciences. One of them consists in the links between science and society and particularly the issue related to the legitimacy of the scientific expertise evolving in a context of institutional crisis. From the communication sciences point of view, the evolution of the experts' legitimacy has never been analysed in the local media discourses. We built a corpus of 1600 articles from the local media LINFO.RE about the theme of shark risk, from 2011 to 2017. We studied this corpus qualitatively through an analysis grid made from argumentation and controversy theories. In addition, we led a quantative analysis in order to establish the frequency of appearance of discourses about science in relation to the total number of publications about the shark risk. An evolution of the legitimacy of scientific experts has been demonstrated with different turning points of qualifications / disqualifications according to the dynamics of the social context, the actors involved, and their arguments. The number of articles written about the shark risk showed peaks of publications in September 2011, August 2012, July 2013 and April 2015, more often following shark attack events. The frequency of appearance of discourses about science showed a variation in the media coverage according to the arrival of new disqualifying arguments, the publication of expertise reports, or a shark attack occurrence. Our study explores how the scientific discourses circulate in the social field and how they can be transformed and reappropriated by the different actors involved in a socio-scientific controversy. The case of media coverage of "shark crisis" in Reunion Island allows us to discuss the dynamics of the scientific experts' legitimacy in a socio-historical context.

Keywords: controversy, scientific expertise, shark risk, local media

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SEGA One Health: planning for the future of effective integrated health surveillance in the Indian Ocean

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Twelve years after the eye-opening Chikungunya epidemic in the Indian Ocean (IO), fuelled by ravaging zoonoses (notably Rift Valley fever) and transboundary animal diseases (FMD, AFS), a charter for a One Health Surveillance and Response network (SEGA One Health) was signed by all IO Commission member States. To strengthen health preparedness, the network's activities the past eight years included health events monitoring, regular calls and meetings, support of national surveillance systems, outbreak investigations, and response. The Surveillance and Response Unit of the IOC coordinates and plans for sustainability beyond the next few years. Therefore the network needs to capitalize on its past successes, increase visibility, become more analytical and anticipatory, foster cooperation and synergies between health sectors and include progressively daily health threats such as diabetes and food-borne diseases to strengthen the systems. Digital health information systems are implemented for real-time reporting. Adapted surveillance system evaluations and benefit-cost analysis document the performance. Next to technical issues, sub-regional expertise is mobilised and strategic plans elaborated showing the priorities of countries and how they are anchored in national health plans. Transversal topics emerge like port controls, cross-country quality assurance of laboratories, capacity-building, risk analysis and targeted communication. There is a large untapped potential of One Health to enhance early detection and control of zoonoses. Novel contingency planning with all line ministries and cost-effective transsectoral economics for zoonoses are key elements and can be extended to other sectors such as plant health. AMR as emerging topic can showcase One Health when it considers the environmental interface of human and animal health and human mobility. Rabies is a prime example of added value of cooperation. Climate change via ecosystem instability and new patterns of vector abundance (e.g. Aedes and ticks), and increasing extreme weather events are closely related to epidemics. Remote sensing for early alerts is only sufficient if linked to social contexts and behavioural adaptations. Newly created regional excellence centres acknowledge these future challenges. Sub-regional harmonised actions based on mutual learning for change require institutional and operational partnerships – and buy-in and long-term commitment by States - stipulating governance becoming an overarching topic.

Keywords: surveillance, network, Indian Ocean, One Health, vector borne disease

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*Speaker

Unpacking the controversies around the management and control of the invasive plant, *Rubus alceifolius*, in Réunion Island: preliminary elements for a sociological research

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The perception of invasive plants by citizens is often underlooked in control programs. The management and control of *R. alceifolius,* the giant bramble, highly invasive in Réunion Island, triggered a great debate among the local community and contributed to diverging opinions about the invasive status of the plant. In 2008, a biological control agent, *Cibdela janthina*, a phytophagous sawfly was introduced to control *R. alceifolius* with approval from the French authorities here represented by the state, regional council, ministries, agencies and institutions. The omnipresence of the biological control agent, a blue-metallic looking fly around the island within a year's time did not go unnoticed and aroused great misunderstanding by the public. A high abundance of *C. janthina*, commonly called the "blue fly" raised uncertainties of its impact upon litchi honey production among beekeepers. This concern was broadcasted amongst the local community and it received great media attention. The local press published headlines expressing the opinion of beekeepers who voiced out their concerns on the decrease of their honey production to the French authorities. The controversy was reflected around the release of a biological control agent in Réunion island. The aim of this study was to determine the different perceptions of this biological control programme from the French authorities, the beekeepers and the research centre. The emergence of the transformation of disputes was selected to determine the rationale behind the controversies on the biological control programme. The available data analyzed were newspapers, scientific committee meetings reports, decrees and orders. Surveys were also undertaken to understand the various point of views which brought about disputes as part of the biological control programme. The results showed that weak communication and involvement of beekeepers prior to the release of the biological control agent have generated discontentment. The none-involvement of beekeepers during the scientific decisions later generated controversies. The research centre was requested to investigate on the issue of the reported decrease in honey production and concluded that *C. janthina* had no link with honey production. The research centre has later collaborated with professional beekeepers, as allies, to undertake the study.

Keywords: beekeepers, biocontrol, media, perception

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[*] Speaker

Sacred groves as habitat islands: biodiversity conservation through cultural practices

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Sacred groves occur worldwide, and are community-managed forests that are protected due to cultural traditions. These groves harbor important natural resources, including diverse flora and fauna, as well as springs. Some of the sacred groves are considered home to local gods. The sacred groves are often fragmented habitat islands within a landscape mosaic of agriculture and human development. A multi-year, multi-site research programme on sacred natural sites is underway. Results will be presented from research in Ghana in 2006, India in 2009-2010, and Sierra Leone in 2012. A qualitative, ethnographic research methodology was used, including open-ended interviews. A similar semi-structured questionnaire was used in all three research locations to interview residents about natural resource use, rules, and belief systems regarding local sacred groves. Results indicate that management approach and level of community involvement are linked to effectiveness of site protection and community attitudes. Societal traditions are key to the continued protection of the groves. In some cases, changing religious traditions and high demands for resource use have resulted in the reduction or loss of groves. However, culturally protected sacred sites can still play a role as key biodiversity conservation areas if community conservation traditions are supported. The groves' cultural significance and local management help ensure the future of these forested habitat islands that represent key remaining biodiversity conservation areas.

Keywords: forest conservation, social science, indigenous and community conserved areas, traditional conservation practices, CBNRM

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How long would it take to recover the number of bird species lost due to humans in New Zealand?

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People sometimes believe that, if left undisturbed, nature will quickly recover to its original state. If ecosystems on islands were left alone, how long would it take to recover the number of species lost due to anthropogenic activities? While the number of extinct or threatened avian species has often been quantified, the macroevolutionary consequences of human impact on island biodiversity have rarely been measured. We estimate the time it takes to regain the bird diversity that has been lost or is under threat due to anthropogenic activity in a classic example, New Zealand. Half of its bird species have gone extinct since humans arrived and a large proportion are threatened, including entire lineages forming highly distinct branches in the avian tree of life. Using paleontological and ancient DNA data, we compiled the first complete phylogenetic dataset of a large insular terrestrial avifauna. We extend the maximum-likelihood method DAISIE developed for island biogeography to allow for the conspicuous fact that many of New Zealand's birds are evolutionarily isolated, and use it to estimate natural rates of speciation, extinction and colonization. Simulating under a range of extinction scenarios, we find that it would take at least 40 million years (Myr) to recover the diversity lost since human colonization of New Zealand and up to 10 Myr to return to today's levels if currently threatened species go extinct. This study puts into macroevolutionary perspective the impact of humans in an isolated fauna and reveals how conservation decisions we take today will have repercussions for million years to come.

Keywords: Palaeontology, Evolution, Phylogeny, Extinction, New Zealand, Conservation, Birds

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Species Interactions / Networks / Trophic Ecology

Contents

The feeding competition between the Mauritian flying fox *Pteropus niger* and the invasive crab-eating macaque *Macaca fascicularis*

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Mauritius has a long history of direct and indirect defaunation, either through hunting and harvesting of native animals, or the introduction of invasive species and logging of native forests. The native forests have become scarce, which has resulted in a conflict between commercial fruit growers and the endemic Endangered Mauritian flying fox *Pteropus niger.* It is the last of the three remaining large seed dispersers that still performs an important ecological function. This function is essential for the passive regeneration of the forest, but it is disrupted by *P. niger's* most important food competitior: The invasive crab-eating macaque *Macaca fascicularis.* Macaques are known to compete with *P. niger* for native fruit, halt native plant reproduction and native forest regeneration and are likely to further fuel the human-wildlife conflict. This study aimed to create a deeper understanding of the impact of introduced macaques on fruit availability to *P. niger* and how this impact affects the ongoing conflict between fruit growers and *P. niger.* Additionally, this study aimed to assess the native plant richness in remnant forests. The study showed that *M. fascicularis* completely halts the reproduction of certain native species by destroying unripe fruit. Furthermore, *M. fascicularis* greatly limits the availability of native fruits to *P. niger*, likely forcing *P. niger* to feed in commercial plantations. However, it is still unclear how big the macaque population is and how much damage to native plants they cause at the island scale, indicating the need for a more in-depth study of the ecology of *M. fascicularis.* Furthermore, the study showed *P. niger* feeds in remnant forests across the island and that a specific plant species can fruit asynchronously depending on its geographic location. More research into these fruiting patterns is needed to understand the role that forest remnants play in providing certain fruits to *P. niger* at a certain time of the year when it would not be available elsewhere. Ultimately, restoring remnant forests and removing invasive macaques could serve as tools to increase the availability of native fruit to *P. niger,* potentially reducing the conflict between *P. niger* and fruit growers.

Keywords: Fruit bat, Feeding ecology, Forest degradation

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*Speaker

Depauperate seed rain but effective recruitment after reinstated dispersal evidence strong impacts of frugivore extinctions on native forest regeneration after natural disturbance

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Frugivore loss may lead to seed dispersal disruption, but this issue has rarely been addressed in the context of tropical primary succession where seed dispersal is a critical step in plant recolonisation. Recent works in several tropical forests suggest that native tree diversity and dynamics are negatively impacted by the disruption of plant-frugivore interactions as a consequence of defaunation. Different limiting factors, i.e. seed predation and competition with dense low vegetation, probably act in synergy with defaunation and must be disentangled to understand biodiversity loss processes. We set up a field experiment on Reunion where most large frugivores went extinct in 1800 and where the Piton de la Fournaise provides a natural experimental design: a historical lava flow bordered on both sides by an old-growth forest. We address the following questions: (1) Is the absence or rarity of native fleshy-fruited (FF) species on the historical lava flow explained by seed dispersal disruption? (2) Are large-seeded FF plants able to grow up once experimentally dispersed from old-growth forest seed sources? We monitored the active seed rain on the historical lava flow in a landscape with a high adult-plant diversity and the growth of four large-seeded trees in a manipulative factorial experiment (seed predator exclosure and fern uprooting) on the historical lava flow where these trees were totally absent. Preliminary results show that the active seed rain was dominated by native anemochorous and alien FF plants; large-seeded FF plants were absent from the seed rain despite a nearby large availability of diaspores; large-seeded trees were able to establish on lava flows, whatever the treatment. The absence of native large-seeded trees and the high abundance of alien small-fleshy-fruited plants in the monitored seed rain demonstrates that present plant-frugivore interactions are diverted for the benefit of non-native invasive plants. The ability of large-seeded plants to establish on the historical lava flow show that dispersal disruption, more than environmental filtering or predation effects, explains the complete absence of these species. Our study emphasizes the fundamental role of seed dispersal loss in ecosystem stable-state shifts and the urgency to restore it through large frugivores rewilding actions.

Keywords: Seed dispersal disruption, Primary succession, Zoochory, Biological invasions, Tropical rain forest

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*Speaker

Seed dispersal by chelonians and the virtually intact Aldabra seed dispersal network

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In recent years, it has become clear that frugivory and seed dispersal (FSD) by chelonians (turtles and tortoises) is much more common than previously thought. Yet, a review and synthesis is lacking. We reviewed published and unpublished records of chelonian FSD, and assessed the role of chelonians as seed dispersers, from individual species to the community level. We found that a substantial proportion of the world's aquatic and terrestrial turtles and a major part of testudinid tortoises (70 species in 12 families) include fruits and/or seeds in their diet, and that fruits of at least 588 plant species in 120 families are ingested and/or dispersed by chelonians. For some chelonians, overall or in certain seasons, fruit may even form the largest part of their diet. Contrary to seed dispersal by lizards, the other major reptilian frugivores, chelonian FSD is not an island phenomenon in terms of geographic distribution. Nevertheless, on islands especially tortoises are often among the largest native terrestrial vertebrates-or were, until humans got there. Aldabra Atoll is one of such islands, and harbours the last native population of giant tortoises (*Aldabrachelys gigantea*) in the Western Indian Ocean. We studied the seed dispersal interactions in the plant–frugivore community of Aldabra Atoll, which is composed of ten frugivores and 37 fleshy-fruited plant species. The network was highly generalised, and giant tortoises were the second most important seed dispersers in terms of the number of interactions. In total, *A. gigantea*dispersed the seeds of at least 20 fleshy-fruited plant species, including large-seeded ones such as *Cordia subcordata*(Boraginaceae) and *Guettarda speciosa*(Rubiaceae). Moreover, we found that the network was most vulnerable to the loss of three particular frugivores, one of them being the giant tortoises. This study highlights the importance of tortoises as seed dispersers –especially as megafaunal ones–and suggests that the many recently extinct giant tortoises in numerous islands around the world had a similarly pivotal role in their communities before being exterminated as the Aldabra giant tortoises.

Keywords: chelonian, seed dispersal, megafauna, networks, community, turtles, tortoises

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Alien ant-disrupted pollination mutualism of a declining island endemic plant varies temporally and is worsened by alien plant invasion

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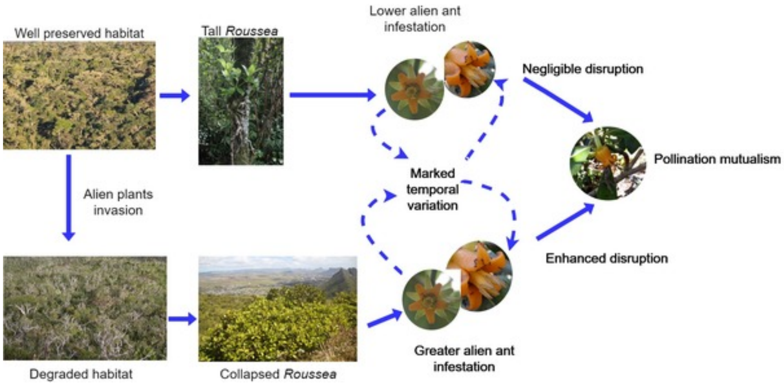

Invasive alien species, through their varied impacts, pose the greatest threat to the thousands of island plants currently considered as highly threatened with extinction. Among these, disruptions of plant-pollinator mutualisms have been receiving increased attention recently. Such threat, however, is likely to vary much spatio-temporally, particularly when driven by alien ants for instance, but this variation remains relatively rarely studied. We examined an endangered Mauritius endemic scrambler (*Roussea simplex*) about a decade after its pollination by an endemic reptile was found to be disrupted by a widespread invasive alien ant (*Technomyrmex albipes*). We quantified alien ants' impact by estimating natural ant-infestations of flowers in four populations and through baiting experiments done at four equidistant heights (50-200 cm) above ground over two consecutive years at two sites. We also characterised the influence of alien plant invasion on the plant's stature. Two alien (*Anoplolepis gracilipes* and *Technomymex albipes*) and one native (*Plagiolepis madecassa*) ant species were found visiting flowers. Only 6.4% of flowers bore alien ants and they occurred predominantly closer to the ground. Mean frequency of infested baits and mean alien ant density per bait varied seasonally and annually and infestations predominated up to 100 cm above ground. *Roussea* plants were about three times taller in well preserved habitats than in invaded ones. New invasive ant species may appear with time and appear to displace pre-existing species and flowers may also provide resources to native ants. The severity of mutualism-disruption varies spatially and seasonally as well as inter-annually and in longer time span. Alien plant invasions increase loss of host plants which causes the scrambler to collapse closer to the ground thereby increasing accessibility of its flowers to alien ants. Alien plant invasion thus amplifies deleterious impacts of invasive ants. Conservation managers should pay attention to spatio-temporal variation in severity of threats that have been documented. It is also important to study documented threats in a broader context to unravel eventual cascading effects. In the current example, to address alien-ant disrupted pollination mutualism, reversing invasive alien plant impact may be the management to adopt instead of controlling the ants themselves.

Keywords: conservation, invasive ants, invasive plants, Mauritius, mutualism disruption, oceanic island

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Effects of exotic pollinators on network structure and ecosystem function

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Exotic species can disrupt plant-pollinator interactions and its ecosystem function. Several studies have found contrasting results regarding the impact of honey bees *Apis mellifera* on native plant-pollinator communities and pollination function. Due to its abundance and generalist behaviour, *A. mellifera* can visit many different plant species, increasing the competition for resources with other native pollinators and modifying the structure of interaction networks. Negative and positive impacts of *A. mellifera* on native plant species include lower pollination effectiveness and replacement of lost pollinators, respectively. Here, we investigate the response of plant-pollinator communities and pollination function to artificially increased *A. mellifera* abundance in an island restoration context. We recorded plant-pollinator interaction and fruit set of native plants during eight months on four control and four treatment sites on the island of Mahé, Seychelles. First results indicate a low impact of *A. mellifera* on global network topologies, yet changes in meso- and micro-scale metrics suggest that specialist plants and pollinators suffer from a higher degree of direct and indirect competition in networks with increased *A. mellifera.* The conservation implications of these findings are two-fold: *A. mellifera* may ensure pollination of rare, more specialised plant species; and *A. mellifera* is likely to outcompete specialised native pollinators. Further research is required to quantify pollination efficacy of *A. mellifera* compared to native pollinators to assess the overall impact of this exotic pollinator on native plant-pollinator communities.

Keywords: ecological networks, pollination ecology, exotic species, ecosystem function, Apis mellifera

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Community-wide difference in floral traits between continental and oceanic island coastal plants

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Oceanic islands usually exhibit lack of large bees and butterflies with long proboscises and dominance of small-sized bees with proboscises in their pollination networks. Such pollinator compositions are known to promote the floral evolution in some oceanic island plant populations, whose ancestors were originally pollinated by large bees and butterflies in continents and continental islands. We recently reported that long-tongued pollinators were more scarce in coastal communities of Izu (oceanic) islands compared to those of the Honshu (continental) island communities in Japan. This scarcity of long-tongued pollinators caused community-level niche shifts in oceanic-island pollinator communities, such that long-tubed flowers were more frequently visited by short-tongued pollinators. However, how have such community-level pollinator niche shifts influenced floral phenotypes in Izu island plant communities are largely unknown. To examine the issue, we compared lengths of the style, stamen and petal (and corolla tube) of 19 dominant species (8, 4, 3 and 4 species with long-, medium, short-tubed and open flowers, respectively) of coastal vegetation between the Honshu and Izu islands: 3 and 5 sites were investigated in the Honshu and Izu islands, respectively. In most long-tubed species, one or more measured traits were significantly larger in the oceanic island sites than those in continental island sites. Conversely, in most medium- and short-tubed species, any or all of the measured traits were significantly smaller in the oceanic island sites than those in the continetal sites. Meanwhile, we found no differences in floral traits of open flowers between continental and oceanic island sites. Thus, we found community-wide differences in floral traits between the continental and oceanic islands in plant with corolla tubes. In some study species, the lengths of floral traits were significantly correlated with the average tongue length of pollinators, suggesting that the pollinator niche shifts might cause the floral phenotype changes in oceanic islands. In other study species, however, floral trait differences between continental and oceanic sites could not be explained by the community average of tongue length of pollinators. Our results suggest that many coastal plant species have flowers adapting to pollinator communities without long-tongued bees and butterflies in oceanic islands.

Keywords: floral traits, pollinator, plant community, phenotypic variation

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Speciation of the sect. Camellia based on pollinator shift in Japanese islands

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The genus *Camellia* (Theaceae) is particularly prevalent in East and Southeast Asia (82-280 species). According to the Flora of China, there are 13 species in the sect. Camellia, of which 12 are found in China (11 being endemic), and only two species, *C. japonica* and *C. rusticana*, are found the in Japanese islands. Most species of *Camellia* have the separated filaments, but the sect. *Camellia* species except for *C. rusticana* and *C. chekiangoleosa* have the connected filaments, which indicates the bird-pollinated flower characteristics to keep large amount of nectar. *C. japonica* occurs in the end of the range of *Camellia* distribution. This species blooms in the winter when insects are absent and have to depend on bird pollination whereas other *Camellias* depend on both pollination, insects and birds. Therefore *C. japonica* might be the most adaptable species to the bird pollination. On the other hand, *C. rusticana* has ancestral traits with not-connected filaments in sect. *Camellia*. We hypothesized that pollinator shift occurred and speciated to sect. *Camellia* from ancestral genus *Camellia*. But *C. rusticana* might to get back to the insect pollination to fit to the snowy environment in Japan. Hence, this study aims to examine the speciation of Japanese *Camellias* based on pollinator shift by comparing the floral morphologies and the genetic differentiations of genus *Camellia*. We compared their morphologies of leaf hypodermis, flower form, petal color, filament color and filament color in the twenty populations and estimate quantitatively the differentiation. The floral traits of *C. japonica* such as filament connection rates, nectar and sugar contents are one of most adapted characteristics for bird-pollination. Genetically, *C. japonica* is newly differentiated species based on MIG-seq and cpSSR, relatively. *C. rusticana* with few common SNPs could not be taxonomically positioned, but it might be an older position in the sect. *Camellia*. In other words, *C. rusticana* didn't return to the insect pollination, but is the ancestral species in the sect. *Camellia*. As for the speciation of genus *Camellia*, the species with bird-pollination traits are not rapidly speciated from their common ancestors but occurred from different phylesis depending on environmental conditions.

Keywords: bird pollination, floral traits, MIG seq, SNPs, cpSSR

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A Fijian rainforest tree requires bats to open its flowers - the strange evolutionary case of chiropteropisteusis, a new pollination system

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Dillenia biflora is an early succession tree of Fijian rainforests with important social and ecological values. Bats of three species trapped for two years on Vanua Levu (2009-2011) carried *D. biflora* pollen, including 70% of individual *Notopteris macdonaldi*, a cave-dependent threatened species. We examined the pollination of 19 trees on Vanua Levu in 2010-11 and 28 trees in November-December 2016 and June-July 2017 on Viti Levu, and determined that the large flowers with globose corollas did not open on their own and aborted when they remained closed (n = 100), indicating that they are not cleistogamous. Only flowers that were opened by bats resulted in fruits, as confirmed by video footage or direct observation (n = 11; all *N. macdonaldi*) and bite marks on corollas. Both self- and cross-pollination by hand after corolla removal produced fruits. Chiropteropisteusis (from the Greek "reliance on bats"- since pollination cannot take place before manipulation by bats) is a unique and previously undescribed pollination system. *Dillenia biflora* is closely adapted to pollination by *N. macdonaldi*, whose dentition appears to be perfectly suited for corolla removal. The evolution of this remarkable strategy, shielding nectar and reproductive organs from heavy rainfall and presumably excluding low-quality pollinators, implies a close overlap in distribution between the cave-dependent bat and the tree. The discovery has already been used to promote bat conservation in Fiji.

Keywords: conservation of bat, plant mutualism, evolution of unique pollination system, Fijian rainforests, pollination by bats, specialisation on bat pollination

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Poster presentations

Atmosphere - biosphere - geosphere interactions

Contents

The critical zone observatory "OZCAR" in La Reunion, targets and future challenges to manage our changing island environments

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OZCAR (Observatoires de la Zone Critique–Application et Recherche or Critical Zone Observatories–Application and Research) gathers French Research Infrastructure (RI) in a national network. OZCAR-RI is a network of instrumented sites, bringing together 21 pre-existing research observatories monitoring different compartments of the zone situated between "the rock and the sky," the Earth's skin or critical zone (CZ), over the long term. These observatories are regionally based and have specific initial scientific questions, monitoring strategies, databases, and modeling activities. Our objective is to present the main targets of La Reunion observatory as a part of Ozcar RI. The critical zone in La Reunion is mainly dependent on the water cycle. Although high tropical volcanic islands exhibit exceptional rainfall, nevertheless the high permeability of young volcanic terrains promotes rapid and deep infiltration of meteoric waters, limiting water availability in the highlands. In those environments, Tropical Montane Cloud Forests (TMCF), intercept the fogs linked to the trade wind inversion and provide superficial water resources. In the context of climate change, the evolution of the trade wind inversion height is likely to modify this system and associated ecosystem services. The consequences concern the future of this exceptional biotope, with high levels of endemism, and the access conditions to water resources for inhabitants of these islands. Initially developed within the experimental watershed of La Rivière des Pluies, we now propose to extend our observations and scientific issues to the scale of the whole island. Hence, in that view, La Réunion Island becomes a single functional unit devoted to the study of complex interactions between hydrosphere, biota and society. Within the Federation for Research OMNCG (observatory of natural environments and global change) part of the Earth Science and Astronomy Observatory (OSU-Réunion), networking among existing local observatories (hydrology, ecology, meteorology and volcanology) should help to promote multidisciplinary research in the long term. This matches the goal of the national network of Zones Ateliers (ZA) and the Horizon 2020 project "eLTER" (European Long-Term Ecosystem and socio-ecological Research Infrastructure).

Keywords: critical zone, eLTER, OZCAR, water cycle, zones ateliers (ZA)

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Biodiversity and Chemistry

Contents

Exploration of natural colorants from Malagasy biodiversity, sources of natural products for the industries

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Synthetic dyes have reached a limit of use with respect to environmental and toxicological problems. The use of dyes extracted from plants as natural colorants for food and non-food applications is considered a promising issue to overcome the ever-rising demand of the consumers to replace their synthetic counterparts. The richness of plant species, the high endemism ratio and the threats related to human activities on this biodiversity classify Madagascar as one of the most important hotspots of the world biodiversity. Dye plants from Madagascar are readily available raw materials that can be cultivated to produce dyestuffs for the production of natural colorants. Because of their chemical and color versatility in their dye profile and a long-term history of well-known uses, these plant species are good targets for the production of a variety of other natural substances. More than 237 dying plants (21% of endemics species, 54% of native species and 25% of introduced plants to Madagascar) have been inventoried in this study, as a result of historical data, ethnobotanical surveys and trials made with some dyers from Madagascar. Despite this richness, the lack of sufficient data about the composition of the dyes and pigments contained in these Malagasy plants and their toxicological impacts limits the development of this sector, both in textile (due to the variability of the shades) as well as in food and non-food applications. With this aspect, colorants which are traditionally extracted from Malagasy dye plants are considered as a new pool of biodiversity to be further explored. Among several applications, ancestral knowledge of natural fibers dyeing and small-scale dye extraction made by craftsmen from Madagascar are recognized worldwide. Nevertheless, this natural plant diversity is not a sufficient value and these important alternative resources in raw materials are starting to disappear. Many other industries and fields may be interested by new natural products with interesting potential applications, such as food coloring and cosmetics. Therefore, the sustainable exploitation of this biodiversity is expected to contribute to its conservation.

Keywords: Biodiversity, dye plants, natural colorants, natural dyeing, Madagascar

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Medicinal plants from Reunion Island as promising source of natural antiviral substances against mosquito-borne flaviviruses

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Zika virus (ZIKV) and the closely related dengue virus (DENV) are mosquito-borne RNA viruses of the genus flavivirus in the *Flaviviridae* family. The medical importance of ZIKV was fully highlighted during the recent epidemics due to its link to severe damage to foetal brain development and neurological complications in adult patients. Dengue fever, caused by 4 virus serotypes, is the most prevalent mosquito-borne viral infection in tropical and subtropical countries including the south-west of Indian Ocean region. Epidemic of DENV-2 is currently taking place in Reunion Island. A worldwide research effort has been undertaken to identify safe and effective compounds to prevent or treat ZIKV and DENV infections. Our data demonstrated that extracts from *Aphloia theiformis* and *Psiloxilon mauritianum*, an edible indigenous and endemic medicinal plants respectively from Reunion island, are potent inhibitors of ZIKV and DENV (4 serotypes). Interestingly, *A. theiformis* and *P. mauritianum* extracts inhibited virus entry in host cells by impairing their attachment to the human cell surface. Electron microscopic observations revealed that organization of flavivirus particles was severely affected by *A. theiformis*. Our results provide novel insights for the potential of Indian Ocean medicinal plants as promising source of natural antiviral compounds in the fight against medically-important arboviruses.

Keywords: Zika virus, Dengue virus, flavivirus, antiviral activity, natural compounds, nutraceuticals, medicinal plants.

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*Speaker

Screening for yeast biodiversity from Réunion island, Madagascar and South Africa. Selection for yeast strain with atypical aroma production and application to natural fruity beer production

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Most of the countries in the southwestern area of Indian Ocean are known to be particularly rich in biodiversity and provide natural habitats for propagation of microorganisms such as yeast. According to specialists in microbial ecology, it is estimated that less than 1% of the existing yeast species has already been described. Therefore we hypothesised that some yeasts from Madagascar, South Africa and Reunion Island could show endemicity and/or display interesting flavouring properties recoverable for the food industry. In this work, we aimed at screening yeast biodiversity from these territories and at evaluating their production of natural flavours in order to select interesting strains for fermented beverages aromatisation. A total of 223 yeast strains were isolated from Madagascar and Reunion Island tropical fruits and from South-African wildlife faeces. Their identification by sequence analysis of the variable D1/D2 domains of the 26S rDNA allowed classifying them into 26 different species. Among them, two isolates from Cape gooseberry (*Physalis peruviana*) and Cocoa beans (*Theobroma cacao* var. *Criollo*) seem to be new species endemic from Madagascar as they display only 97,1% and 97,4% of identity with *Rhodotorula mucilaginosa* and *Candida pararugosa* respectively. The analysis of aromas production profiles of the yeasts was realised by Headspace-Solid-Phase-Micro-Extraction coupled to Gas-Chromatography and Mass-Spectroscopy (HS-SPME-GC/MS). Considering all yeasts, 52 volatiles organic compounds were identified and classified into 5 molecules groups: acids, alcohols, aldehydes, ketones and esters. With 32 different molecules, including high fruity aroma unsaturated esters – such as ethyl-tiglate – *Geotrichum fragrans* (*Sapraochete suaveolens*) appeared as the best candidate to produce high amount of natural fruity aromas. The technological performance of *G. fragrans*, isolated from Dragon fruit (Pitaya), and inoculated at different ratios together with the brewer yeast *S. cerevisiae,* was evaluated in brewing fermentation conditions at the laboratory scale and pilot scale. Results showed that beer formulated with 100% *G. fragrans* displayed less ethanol content and twice more total flavour compounds than standard beer made with only *S. cerevisiae*. This work also demonstrated that wild yeast strains isolated from natural habitats, can generate new biocatalysts to be used to improve the formulation of novel foods.

Keywords: yeast, biodiversity, biotechnology, flavours, beer, fermentation

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A chemotaxonomic study of volatile compounds from 17 Psiadia species endemic to Reunion island and Madagascar

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The genus *Psiadia* Jacq. Ex. Willd. (Asteraceae) includes more than 60 species found in tropical and south of Africa, Madagascar and the Mascarene Islands (Reunion, Mauritius and Rodrigues). It is described in traditional pharmacopeia for the treatment of ailments such as abdominal pain, colds, fevers, as expectorant or in plaster preparation for broken bones in Bedouins. However, few species have been the subject of in-dept phytochemical and biological studies with a view to validating traditional uses and developing a drug. In this context, and in order to contribute to enhance the knowledge of *Psiadia* species from Réunion island and Madagascar, a chemotaxonomic study was undertaken using a metabolomic approach. In phytochemistry, metabolomic is an emerging field of "omics" research that focuses on high-throughput identification and quantification of metabolites. Volatile compounds from 11 species endemic to Réunion and 6 species endemic to Madagascar were studied. Their essential oils were extracted by hydrodistillation and then analysed by gaz chromatography coupled to mass spectrometry (GC-MS) and by gaz chromatography coupled to flame-ionization detection (GC-FID), two of the most currently methods used for caracterizing volatile compounds. The aim was to determine possible similarities or differences in their chemical composition and to identify chemical markers, using multivariate chromatographic data analysis. The results of this study will contribue to raise awareness about the preservation of *Psiadia* species in Réunion and Madagasca and their valorisation in therapeutic area.

Keywords: Psiadia, species, chemotaxonomic, metabolomic, chromatography

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[*] Speaker

Fast identification of bioactive compounds in Psiadia species by a 1H NMR-based metabolomic approach

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The genus *Psiadia* (Asteraceae) is well represented in Madagascar and the Mascarene islands (Mauritius, La Réunion, Rodrigues). The leaves of these species have pharmaceutical interests, being used as decoction for treatment of bronchitis, asthma, colds and abdominal pains... A preliminary screening displayed the antiplasmodial, anticancer and anti-inflammatory potentials of some *Psiadia* species without identification of bioactive compounds. The aim of this study is to fast identify bioactive compounds or family of compounds of *Psiadia* species using 1H NMR-based metabolomics analysis. Orthogonal projections to latent structures discriminant analysis (OPLS-DA) was applied to discriminate active crude extracts and identify the active compounds. The results showed that a polyyne was correlated to the antiplasmodial activity of *P. amygdalina*; methoxylated flavonoids and a coumarin were found to be the active compounds for the anti-inflammatory, anticancer and antiplasmodial activities of *P. dentata*. Finally, the antiplasmodial activity of *P. arguta*, *P. anchusifolia* and *P. lithospermifolia* was attributed to terpenoids.

Keywords: 1H NMR, bioactive compounds, metabolomics, Psiadia

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Acaricidal and insecticidal activities of plants among Réunion island's flora

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La Réunion is among the world's top biodiversity hotspots with an endemic rate approximately of 40%. Due to the tropical climate, the island is subject to manifold crop pests and vector diseases. Among them, Bactrocera cucurbitae also known as the melon fly is considered as the major pest of Réunion island's agricultural activities. On the other hand, the cattle industry is affected by the tick *Rhipicephalus microplus* causing enormous losses in milk and hide production. With the purpose of discovering new biocidal natural extracts, several plants from the Réunion island's flora were also explored. The essential oil (EO) of *Peperomia borbonensis* was evaluated by using a filter paper impregnated against the melon flies. The EO characterized by a high predominance of phenylpropanoids compounds with myristicin (39.5%) and elemicin (26.6%) as main components showed a LC50 and LC90 of 0.23 mg/cm^2 and 0.34 mg/cm^2. The median lethal time (LT50) was also determined to compare the toxicity of EO and the major constituents. The EO was the most potent insecticide (LT50= 97.97 min, SE = 1.72), followed by the mixture of myristicin and elemicin (1.4:1) (LT50= 126.84 min, SE = 2.11). Against *Rhipicephalus microplus*, the acaricidal activity was evaluated using the modified larval packet test (LPT). At a concentration of 5 %, the leaves of *Peperomia borbonensis* and the bark of *Zanthoxylum heterophyllum* extracts have showed a mortality rate of 100%. *Monimia rotundifolia* (65.7% of mortality) showed a medium activity and *Psiadia amygdalina* leaf extract had weak acaricidal activity with 31.8% of mortality. These plant extracts exhibited biocidal activities that were not described in the literature and that are congruent with traditional uses for some of them. This emphasize the fact that exploring Réunion island biodiversity could lead to the discovery of new active molecules and the valorization of little known plants.

Keywords: acaricidal, biodiversity, insecticidal, plant extracts, Réunion island

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Biogeography

Contents

Intraspecific diversification with polyploidization of *Clerodendrum trichotomum* s.lat. in the Japanese archipelago

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The Japanese archipelago is a long island arc including more than 3000 islands and located in east edge of Asia. Its flora is basically originated from Eurasian continent while more than 2500 endemic vascular plants species have been recognized in the Japanese archipelago. *Clerodendrum trichotomum s.lat.* is a common shrub and widely distributed in East Asia. Previous study reported the Chinese var. *trichotomum* is diploid in wide area of China whereas two Japanese individuals have been reported as tetraploid. In the satellite islands of the Japanese archipelago, three local taxa have been recognized: *C. trichotomum* var. *yakusimense*, var. *esculentum* and *C. izuinsulare*. The ploidy levels of the three taxa have remained unclear. To reveal the differentiation process in Japanese *C. trichotomum s.lat.* with polyploidization, we analyzed ploidy levels and genetic relationships among the four taxa. To know the ploidy levels of each taxon, chromosome counting, flow cytometric analysis and microsatellite genotyping were carried out. To know the genetic relationships among four taxa, 223 SNPs on nuclear genome and 1325 bp on chloroplast genome were analyzed for 185 and 79 individuals, respectively. *Clerodenerum trichotomum* var. *esculentum*, *C. izuinsulare* were diploid ($2n = 52$) whereas Japanese *C. trichotomum* var. *trichotomum* and var. *yakusimense* were tetraploid ($2n = 104$). The Japanese diploid taxa were distributed only in southern edge of the Japanese archipelago. A chloroplast haplotype, A1, was shared between *C. izuinsulare* and Japanese var. *trichotomum*, and B9 was shared between var. *esculentum* and var. *yakusimense*. On nuclear composition, the Japanese tetraploid taxa was not distinguished from Chinese diploid var. *trichotomum*. On the other hand, the Japanese diploid taxa each showed unique composition. The results of ploidy levels suggested that the diploid taxa in the satellite islands were not originated from the Japanese var. *trichotomum*, rather remnant lineages in the Japanese refugia. Discrepancy between the results of chloroplast and nuclear genetic composition suggested that the Japanese tetraploid taxa were established by complicated processes involving both Chinese and Japanese diploid lineages.

Keywords: Japanese archipelago, Clerodendrum, polyploidization, MIG seq

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Latitudinal and longitudinal variation of body mass of some Malagasy understory birds

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Even though considerable data exists on the body mass of Malagasy birds, to date no analysis has been published on variation along latitudinal or longitudinal gradients. According to Bergmann's Rule, animals increase in body size with increasing latitude or the inverse with declining latitude. The main intent of this study was to test this biogeographical rule with regards to Madagascar, the 4th largest island in the world, and with notably heterogeneous climatic conditions. Data on the body mass of six Malagasy forest-dwelling bird species widely distributed across Madagascar were employed in this analysis, based on animals captured during field surveys, and in different ecological zones. Results indicate that body mass *Newtonia brunneicauda* and *Copsychus albospecularis* changed along a latitudinal gradient in the eastern region. In contrast, variation in body mass of *Bernieria madagascariensis*, *Monticola sharpei*, *Terpsiphone mutata* and *Xanthomixis zosterops* was more pronounced along an east-west longitudinal gradient as compared to a north-south latitudinal gradient. The bioclimatic conditions influencing Malagasy forest ecosystems change more dramatically along longitudinal gradients (which also includes an important elevational component), as compared to latitudinal. Hence, the body mass of eastern humid forest-dwelling species is notably similar across a north-south gradient spanning nearly 1400 km and does not follow, at least in a simplified form, Bergmann's Rule. A larger sample of species needs to be considered in future analyses for verification of the preliminary conclusions presented here.

Keywords: Malagasy birds, body mass, longitudinal gradient, latitudinal gradient, variation

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*Speaker

Multiple colonizations and parallel radiations of Peperomia (Piperaceae) on the Hawaiian islands suggest context-dependent role of niche preemption in diversification on oceanic islands

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Niche pre-emption, where earlier arriving lineages may develop ecological and adaptive advantages and thus inhibit the ecological and evolutionary success of later arriving lineages, has been argued to play a dominant role in the assembly of oceanic island floras. On the Hawaiian Islands, for example, most of the iconic and species-rich groups of the archipelago (e.g., silverswords, lobeliads) are each derived from evolutionary radiations from single colonist lineages whereas many species-poor genera are derived from multiple colonization events. Here, using a molecular phylogeny of *Peperomia* (Piperaceae) in the Pacific, where it is one of the most species-rich angiosperm groups, we reveal a unique history of colonization and diversification in contrast to other elements of the Hawaiian flora and expectations under niche pre-emption. To better resolve the evolutionary relationships of Pacific taxa, we sequence full chloroplast genomes for half of species in the Pacific (including all native Hawaiian species), using a genome skimming next-generation sequencing approach. Using this phylogeny, which we date using a fossilized birth death model of the Piperales, we find that the Hawaiian Islands have been colonized by at least four separate *Peperomia* lineages from the Neotropics, with most diversification occurring relatively recently in the Pliocene. Most importantly, while the Hawaiian flora provides examples of spectacular radiations from single colonist ancestors (e.g., silverswords, lobeliads), we show that endemic *Peperomia* taxa on Hawaii are derived from radiations from two distinct colonists, the first documented case among species-rich plant groups of the Hawaiian flora. The diversification of two clades in parallel suggests that ecological release due to the paucity of large native vertebrate herbivores and the relatively open understoreys of Hawaiian wet forests may have allowed both lineages to flourish, and adds a new twist to our understanding of how oceanic island floras assemble.

Keywords: genome skimming, Pacific biogeography, diversification, oceanic island assembly, niche, preemption

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[*] Speaker

Insular biodiversity: biogeography of reptiles of Malagasy near-shore islands

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Little is known about most vertebrate groups living on the near-shore islands of Madagascar, including reptiles. On the basis of available specimens from recent field research of different near-shore islands and data from the literature, we compiled reptile species lists for 46 islands. Most of these islands are located in northern and western areas of the marine coastal zone of Madagascar. Ten sites from these islands were selected based on their size and nautical distance from the main island. In total, 119 reptile species, of which 115 are considered as naturally occurring, were documented on these near-shore islands. Most of the species are widely distributed across the main island, only a few species are locally endemic at the level of a near-shore island of some archipelago. The analysis of the relationship between species richness, island size, and distance to the mainland, revealed that species richness of reptile communities is correlated to island size, but not with the distance from the mainland. Therefore, the classical MacArthur & Wilson island biogeography theory is only partially supported. At a finer scale, reptiles living on near-shore islands with similar climatic and habitat conditions to the nearby main island have close faunal affinities. Given that these near-shore islands, are home to endemic species, as well as several undescribed and recently discovered species, they represent a refuge for these taxa and further biological investigation are needed during favorable seasonal periods to advance a greater understanding of the evolutionary patterns, which are crucial for management and conservation.

Keywords: near, shore islands, distance, diversity, size, Madagascar

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Increasing knowledge on the threatened endemic bryophytes from Macaronesia: main threats, priority habitats and the role of Natura 2000

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Macaronesia is one of the 25 world biodiversity hotspots and harbour an exceptionally high diversity of bryophytes, containing ca. 796 taxa, corresponding to ca. 38% of the European species richness. In order to develop the European Red List of bryophytes, the status of a selection of 176 species occurring in Macaronesia (all three northern archipelagos) and the Atlantic fringe of Europe was assessed using the IUCN Red List Categories and Criteria. Fifty Macaronesian endemic bryophyte species were evaluated and 38 classified in threatened categories (seven Critically Endangered [CR], 21 Endangered [EN], and 12 Vulnerable [VU]) and 10 additional species were considered in the Near Threatened (NT) category. The habitat preferences, main threats, and occurrence in the Natura 2000 conservation network of 50 endemic species were analysed. We considered the assessment under six broad habitats: Laurel forests, Shrubland and Grasslands, Coastal areas, Water habitats, Rocky areas (including high mountain) and Caves. An analysis of the bryophyte distribution by habitat revealed that Laurel forests comprise the highest number of threatened taxa (1 CR, 21 EN, 11 VU). The remaining habitats also provide shelter for conservation concern species, namely Rocky areas (1 CR, 1 EN, 5 VU), Shrubland and Grasslands (2 CR, 2 EN, 4 VU), Water habitats (3 CR, 4 EN, 1 VU), Caves (4 EN, 2 VU), Coastal areas (2 CR). The main threats to the conservation of species were categorized into: Habitat loss, Habitat degradation, Climate change and Geological events. Climate change and Habitat degradation affect all the endemics, revealing similar patterns for the Macaronesian archipelagos. Habitat loss and geological events are most striking in the Azores. The main threats vary across the different habitats, affecting mainly the Laurel forest, followed by the Water habitats, Rocky areas, Shrubland and Grasslands, Caves and Coastal areas. The effectiveness of the Natura 2000 network to protect endemic species is high, although additions should be necessary mainly in some areas of the Azores archipelago. Macaronesian endemic bryophytes are under severe pressures and should be protected, either by the improvement of habitat conditions, species management, and the recognition of their value in the ecosystems.

Keywords: IUCN Red List, endemic bryophytes, Macaronesia, main threats, habitat preferences

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Centres of endemism in the bryoflora of southern Africa

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Ongoing climate changes may cause alterations in the ecosystem's water balance and will most likely have a negative impact in several species. Therefore, cataloguing endemic taxa is an important initial contribution because it provides the basis for their conservation. To determine which areas might be considered for priority conservation action and species recommended as priority for Red-List evaluations using IUCN criteria, it is important to identify centres of plant diversity and endemism. There are three principal regions of vascular plant diversity and endemism in southern Africa, viz. the Succulent Karoo, Cape Floristic, and Maputaland-Pondoland Regions. This paper deals with identifying and describing the centres of bryophyte endemism in the Flora of southern Africa (*FSA*) region. Diversity patterns in bryophytes do not always coincide with those of vascular plants and other organisms, and therefore bryophyte hot-spots should be determined separately to facilitate the conservation of these early land plants because they have different substrate and habitat requirements. Recently it has been determined that annual rainfall and habitat heterogeneity are good predictors of moss species richness in the southern African region and that moss diversity in southern Africa is greatest in the Cape Fold Mountains of the southwestern Cape, and the Drakensberg of KwaZulu-Natal, Mpumalanga and Limpopo. The geographical distribution data used in this study includes data recorded directly from specimen labels in PRE and associated BODATSA database. The taxa that are restricted to *FSA* (endemic element) are identified. The percentages of endemism at the family, genus and species level are calculated. Endemic species per quarter degree grid square (QDS) are mapped and areas of high diversity of endemics described as centres of endemism. The centres of bryophyte endemism are compared to known centres of seed plant endemism and to centres of moss diversity to determine to what extent they overlap. The levels of bryophyte endemicity on the subcontinent is compared to endemicity in the Mediterranean region (Macaronesian islands) and Indian Ocean islands (Mascarene Islands) to determine the patterns observed. Currently the *FSA* bryoflora comprises 190 endemic bryophytes.

Keywords: Bryophytes, centres, diversity, endemism, southern Africa

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Viral infection dynamics and diversity in two Réunion free-tailed bat colonies

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Bats are natural hosts of many infectious agents. During the last decades, bat-borne viruses were associated with worldwide health crisis, underlying the need to better assess virus epidemiology in bat populations. The aim of this study was to investigate the infection dynamics and diversity of Coronaviruses and Astroviruses, two zoonotic viruses with emerging potential, in two colonies of free-tailed bat (*Mormopterus francoismoutoui)* endemic to Reunion Island. A total of 634 feces samples were collected during a breeding season, and screened for the presence of virus polymerase gene using specific PCRs. Coronaviruses and Astroviruses were detected in both bat colonies, with significant differences in the proportion of positive individuals between viruses: 18% ± 4% for Coronaviruses and 2% ± 1% for Astroviruses. We also observed a significant variation in Coronavirus prevalence over time, with two major peaks of infection, corresponding to later pregnancy and to the first month after parturition. Sequence analyses suggested that only one genotype of Coronavirus may circulate. In contrast, we found a large diversity of Astroviruses phylogenetically related to avian Astroviruses which might suggest potential host shift between bats and birds, locally. This study raises many questions and underlines the need to decipher the drivers of virus transmission in bat colonies in order to better assess the potential risk of spillover and emergence to human populations.

Keywords: bats, astrovirus, coronavirus, infection dynamics, host shift

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Inventory of Mayotte echinoderms: methodology and perspectives

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The western Indian Ocean remains a poorly known region in terms of marine fauna : many important groups of invertebrates such as cnidarians, ascidians, sponges or echinoderms, remain mostly unexplored between Mozambique and the Red Sea. Meanwhile, growing pressures such as climate change, massive coral bleaching, anthropogenic pollutions, overfishing and poaching render the knowledge of this region's biodiversity of paramount importance. This is the context in which we decided to launch in 2016 a detailed inventory and assessment of the echinoderm fauna in Mayotte island, situated between the Union of the Comoros and Madagascar, in order for it to serve as a milestone for biogeography, ecology and conservation in the region. This work, aiming at exhaustiveness, used a mixed methodology to achieve an inventory as complete as possible. Field observations were conducted all along the coast of Mayotte, covering the main marine habitats. When possible, these field studies were replicated at different times of the day, day and night, and at different seasons. Field investigations included both snorkeling at very shallow depths and scuba diving as deep as 50 m, with additional deep dives as deep as 120 m by technical divers. Thirty-one main sites were completely investigated, and tens of others were visited. Additionally, we reviewed and compiled scientific literature from the region to constitute a list of species recorded for Mayotte or potentially present. This was completed by investigations in the MNHN, local institutions and private collections, as well as underwater pictures of the local underwater photographers community. We established a list of 168 species of echinoderms in Mayotte, including 78 new records and 3 probable new species, along with ecological and abundance data. These results increase the geographical range of many species (some being previously considered as Pacific endemics) and adds new information about the ecology, behavior and diet of many poorly known species.

Keywords: Echinodermata, Mayotte, biogeography, marine fauna inventory, marine ecology

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*Speaker

GIFT – A Global Inventory of Floras and Traits for island biogeography

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To understand the processes that shape the assembly of island floras, solid baseline knowledge about the species composition and environmental characteristics of islands is needed. These baseline data can be integrated with functional and phylogenetic information to gain a deeper understanding of island biogeographical processes such as colonization and speciation-extinction dynamics. A valuable source of species distributions and traits are regional Floras and checklists, which contain highly curated information about the species composition of a clearly defined area and often descriptions of species' floristic status and functional traits. Here we present our recent efforts to mobilize this information for macroecological and biogeographical analyses in the GIFT database, the Global Inventory of Floras and Traits (http://gift.uni-goettingen.de). GIFT integrates plant distributions, functional traits, phylogenetic information, and region-level geographic, environmental and socio-economic data. It currently holds species lists for 2,893 regions across the world, including _˜315,000 taxonomically standardized species names (i.e. c. 80% of all known land plant species) and _˜3 million species-by-region occurrences. Islands are a priority in GIFT, being represented by 1,845 checklists that cover 82,672 species, 51,658 of which are restricted to islands. GIFT holds additional information for each island, e.g. on the geological origin and age, geographical isolation, area, past and present climate, the geographic setting during the Last Glacial Maximum, and the archipelago each island belongs to. GIFT also takes advantage of the wealth of trait information in the regional Floras, holding information for 83 functional traits and more than 2.3 million trait-by-species combinations. Particularly high coverage is achieved for categorical traits such as woodiness (_˜233,000 spp.) or growth form (_˜213,000 spp.). As such, GIFT allows tackling questions at the forefront of island biogeography, for example, how functional traits impact colonization success, or which lineages diversify on oceanic islands.

Keywords: Assembly processes, Functional traits, Plant checklists, Species composition, Vascular plants

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[*] Speaker

Long-term persistence within Antarctica's most speciose plant genus, the moss Schistidium

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Mosses are the dominant terrestrial vegetation of Antarctica, occurring across most the small 'islands' of ice-free ground that characterise the continent. The genus *Schistidium* (Grimmiaceae, Bryophyta) is the most species-rich plant genus in the Antarctic, as well as containing most Antarctic endemic species. We assessed the diversity, richness and relative age divergences within all the species representing *Schistidium* with material available from Antarctica. We applied phylogenetic and molecular dating methods based on nuclear ribosomal Internal Transcribed Spacer sequences. We additionally investigated the continent-wide genetic diversity within the most common Antarctic representative - the endemic species *S. antarctici* - and performed preliminary phylogenetic analyses of specimens from the total distribution of the bipolar species *S. rivulare*. Most Antarctic *Schistidium* species were clearly genetically distinct, and interspecific divergences took place at least _˜1 Mya. The widespread endemic species, *S. antarctici*, diverged from other Antarctic congeners in the late Miocene. Within *S. antarctici* the presence of several distinct clades separating the eastern Antarctic Peninsula and Scotia Arc islands from the western Antarctic Peninsula and all continental locations suggests that the rugged spine of the Antarctic Peninsula forms a strong barrier to gene flow. Increased genetic diversity in the northern Maritime Antarctic may support this region hosting glacial refugia. The data obtained suggest likely *in situ* persistence in Antarctica for all endemic *Schistidium* species over at least one million years. The Miocene origin of *S. antarctici* reveals the oldest extant plant species currently known in Antarctica. These data provide strong support for the hypothesis of Antarctic vegetation survival *in situ* in refugia through multiple glacial periods.

Keywords: bryophyte, polar, biogeography, biodiversity, survival, Antarctic, moss

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The importance of small islands in maintaining biodiversity: species-area relationship and structural connectivity. An example from the Western Mediterranean

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The Mediterranean region is an important biodiversity hotspot, with several thousands of small islands and rocks. These numerous islets and rocks, even if characterized by a few square meters and limited resources, host endemic species with populations often composed of few individuals. In order to test the importance of such islets as biodiversity reserves, we analysed the species-area relationship and structural connectivity of the herpetofauna of the "La Maddalena Archipelago National Park" (NE Sardinia, Italy) consisting of about 80 islands, islets and rocks hosting up to 17 herpetological species. We considered 51 islands and tested the relationship of species richness with several environmental factors (area; number of unique habitats; topographical variables; and distances of each island to Sardinia, to the nearest island, and to the nearest big island) using different methods Generalised Additive Models and connectivity analysis using graph theory and software Conefor 2.6. Each method was performed running several comparisons: a) considering all species; b) excluding species in "transit"; c) including only autochtonous species; d) including species present on islands of five different area categories; e) excluding, in turn, all Amphibia; all Scincidae; all Geckonidae; the four Lacertidae; all Colubridae; f) excluding one species in turn. Variables with higher correlations were number of unique habitats, and maximum and the standard deviation (SD) of altitude. Except for species present on islands belonging to the three smallest area categories, all models selected the same variables: SD ruggedness, area, number of unique habitats, and mean and maximum altitude. When excluding Sardinia, the islands contributing the most to the global connectivity of the network are the major islands La Maddalena, Caprera and Spargi but the small islands were of key importance in maintaining the general connectivity and endemicity of the network with the endemic gecko *Euleptes europaea*, and the Tyrrhenian Wall lizard *Podarcis tiliguerta* a species characterized by high genetic diversity. Conservation measures should not overlook the importance of small islands due to their value in preserving biodiversity.

Keywords: connectivity analyses, generalized additive model, herpetofauna, islands, Mediterranean.

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[*] Speaker

Biodiversity and biogeography of soil protists in continental and oceanic islands

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Global diversity patterns have been studied for more than two centuries of plant and animal, but much less for soil organisms and only a small proportion of the diversity of terrestrial protists is known and referenced in databases. Besides improving reference databases, our main goal is to test how far basic biogeographical rules developed for macroscopic organisms apply to microbial eukaryotes with special focus on protists, and especially on testate amoebae. Our key questions are: Do the taxonomic richness, the endemicity, the endemic richness, the phylogenetic diversity and the age of endemic species (as inferred from phylogenetic distance) vary in relation to land surface area, island age, distance to the nearest continent, elevation, land-use, and organism size within given taxonomic groups. To answer these questions, soil samples in both hemispheres will be collected along elevation gradients in four islands/archipelagos with increasing distance to continents (Canary-Réunion-Azores-Hawaii), two archipelagos of large islands/subcontinent with contrasted distance to the nearest continent (Japan-New-Zealand), and two distant continents of different paleogeographic origin (Laurasia: Western Europe, Gondwana: Chile). By using different HTS methods (e.g. Illumina, PacBio) and Sanger sequencing for different gene regions, we will study the diversity of i) all soil micro-eukaryotes at coarse taxonomic level, ii) selected taxa of phylogenetic interest, iii) Hyalospheniidae and/or Euglyphida testate amoebae and Amobozoa at the species level, and iv) Hyalospheniidae and Euglyphida testate amoebae by microscopy and DNA barcoding. We welcome applications from MSc students to do their thesis work on this project!

Keywords: microbial biogeography, biodiversity, long, distance dispersal, endemism, micro, eukaryotes

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*Speaker

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Edaphic habitat islands in quartz fields of South Africa – a model system for island biogeography?

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The Equilibrium Theory of Island Biogeography has commonly been applied to habitat islands, as the share fundamental characteristics with true oceanic islands (e.g. isolated areas regarding species distribution). Indeed, to which degree both systems are comparable recently has been addressed as one of the 50 open questions of island biogeography. While true islands are surrounded by water, the matrix in between habitat islands varies strongly in terms of type and permeability. Despite variables such as island area, topography and geographic isolation, it is therefore necessary to define environmental isolation by including information on the matrix quality in studies on habitat islands. In this study, we use a combined approach of remote sensing techniques, community ecology and island biogeography to quantify drivers of different aspects of taxonomic and functional diversity as well as endemism in a unique system of edaphic habitat islands. We identify habitat island structure, heterogeneity and diversity as well as environmental and geographic isolation based on satellite image classification and a subsequent ground truth vegetation survey. We quantify the processes and drivers at different scales (community, island, landscape) and on different levels of organization (species and functional). Our study area is located in the South African Succulent Karoo, a biodiversity hotspot with outstanding numbers of vascular plant species. Our archipelago-like study system of quartz fields contains high numbers of succulent dwarf shrub species, of which many are local endemics and highly adapted to a small scaled mosaic of habitats within the quartz fields. We will address the following research questions: What drives the assembly processes of the quartz field flora along steep environmental gradients (community scale)? Do quartz island characteristics such as area, habitat diversity, environmental heterogeneity and isolation explain plant diversity, plant traits and niche characteristics on quartz fields (island scale)? What is the relative contribution of habitat islands on the quartz fields to different scales of diversity (landscape scale)? In sum, we present a conceptual overview of our quartz island project from an understudied, yet uniquely diverse area that aims at explaining patterns of diversity and endemism across scales.

Keywords: habitat island, environmental isolation, habitat amount hypothesis, quartz islands, plant endemism

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Regional patterns of vascular species richness in a subarctic island and the role of environment and history

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Most groups of terrestrial organisms show a trend of decreasing species richness from the tropics to polar regions. Three sets of hypotheses have been proposed to explain these patterns, related to climate (temperature and rainfall), spatial heterogeneity (topography/habitat) and historical and/or evolutionary causes. We used 10 × 10 km distribution maps of vascular plants in Iceland and k-means cluster analysis and Principal Components Analysis to explore the role of climate (temperature, precipitation, snow cover), topographic heterogeneity and disturbance regime as determinants of species richness. Iceland is a large (103 000 km-2) island in the North-Atlantic just below the Arctic Circle. Other high-latitude oceanic islands are all much smaller but in a comparison of islands with similar isolation and climate, Iceland stands out in having no vascular endemics and in its relatively low species richness. Given its subarctic location, biogeographic patterns might be expected to reflect the latitudinal gradient from the warmer and moister south to the cooler and drier north. Indeed, earlier work has demonstrated that temperature-related variables and topography were the key environmental correlates associated with floristic clusters of vascular plants. Patterns of vascular species richness however, do not show a south-to-north cline. The northernmost lowlands, the only part of Iceland classified as Arctic and now largely uninhabited, turn out to be species rich relative to other regions. The available data are unable to explain this satisfactorily. A second regional-scale pattern is the relative paucity associated with the active volcanic zone that runs as a broad belt across Iceland, oriented N-S in the north and NE-SW in the south. Iceland experiences on average 20 volcanic episodes per century, some accompanied by heavy tephra deposition and large lava flows. We suggest that the combination of high frequency, high magnitude and spatially extensive disturbances account for the low species richness of this zone.

Keywords: vascular species richness, subarctic, topographical heterogeneity, climate, disturbances

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*Speaker

First genus-wide phylogeny of the genus Ramalina (lichenized Ascomycota) sheds light on the endemic diversity in Macaronesia

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Ramalina, c. 200 species known worldwide, is one of the most diverse genera of lichen-forming fungi. The large size of most species and their usual straw color make *Ramalina* an easily recognizable group of macrolichens. Several areas with high levels of diversity and endemism are known, *i.e.* Australasia, East Africa, Baja California, and Macaronesia. The last case is paradigmatic, with c. 40 known species, more than 50% of them are endemic, including two putative inside radiations (the *R. decipiens* and *R. bourgaeana* groups), and at least seven examples of single-island endemics, a rare distribution pattern in lichen-forming fungi. Knowledge about phylogenetic relationships within the genus is scarce

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and any hypothesis about the origin of Macaronesian endemic species has been precluded due to the sparse taxa sampling and the poorly supported phylogenetic hypotheses. In this study we built a new phylogeny for the genus *Ramalina* based on a thorough survey in Cape Verde, Canary Islands, and Madeira archipelagos; genus-wide taxa sampling including species from all continents and new informative markers obtained from the comparison of five genomes sequenced from axenic cultures. This approach allowed us 1) to infer the number of independent colonization events, 2) to unveil interesting biogeographic connections for the Macaronesian *Ramalina, 3)* to delimit the in-situ radiations, and 4) uncover hidden diversity, increasing the number of endemic species in the area.

Keywords: Canary Islands, Cape Verde, colonization events, endemism, lichen, forming fungi, Madeira

Origin and diversity of an emblematic Mascarene hygrophilous lineage: the case of filmy ferns

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Also known as "filmy ferns" due to their delicate, one-cell thick lamina, the Hymenophyllaceae are abundant in hygrophilous forest of the Mascarene islands, where they are usually found as epiphytes or lithophytes. They are also one of the most diversified fern families in the archipelago, but with few endemic species (only one known before this study). With a view to re-assessing the diversity, endemism and origin of this family in the Mascarenes, we gathered data from floras, literature, collections and field investigations. In parallel, we reconstructed dated phylogenies for several genera of the family. Our updated checklist recognizes 22 species, 2 local varieties and 1 new forma. The most diverse genera are *Hymenophyllum* (8 species, 1 forma) and *Crepidomanes* (7 species, 2 varieties), followed by *Didymoglossum* (3 species), *Abrodictyum* (2 species), *Polyphlebium* and *Vandenboschia* (1 species each). Based on the reconstructed phylogenies, we infer multiple colonization events of filmy ferns in the Mascarenes, the vast majority of which are from Madagascar. To the previously single endemic species (*Didymoglossum barklyanum*), we add at least three species: *Hymenophyllum fumarioides* (syn. of *H. tenellum*), *H. hygrometricum*, and *H. inaequale*. All these endemics appear to be of anagenetic origin. Of the 22 Mascarenan species, 19 are colonial epiphytes or lithophytes colonizing their substrates. Filmy ferns are most abundant in the megatherm zone (_˜450–600 m), with a second elevational distribution mode in the mesotherm zone (_˜1,200–1,500 m), and a small third one close to the tree-line (_˜1,950–2,100 m). Although we observe no cladogenesis event, our study reveals that speciation has been underestimated for the family, in the archipelago as well as in the whole Indian Ocean region. This raises the need for further taxonomic studies in the family. The preponderance of epiphytic taxa, in comparison with Madagascar and continental areas, is likely related to their gametophyte morphology, which would facilitate colonization and establishment on oceanic islands. Finally, the unexpected occurrence of several species in ravines of semi-dry forests, notably one *Crepidomanes* variety restricted to the area, support the importance to protect these threatened habitats along with lowland rainforests.

Keywords: Hymenophyllaceae, Mascarenes, phylogeny, epiphytism, elevation

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Biogeography of Hermannia (Malvaceae): islands, sky islands and montane barriers

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A lack of revision due the challenges associated with a large and obscure genus have rendered *Hermannia* an obscurity and at best a curiosity. A 12 year revision of the genus, published as a PhD, reveal this to be one of the most exciting genera in Africa. With over 300 species, over 100 of which have been discovered during the PhD, there are continually new species being discovered. The 5th largest genus in the Cape Floristic Kingdom and a "Cape Clade", an analysis of the biogeography of *Hermannia*, especially in conjunction with phylogeny and climate, reveals some neat patterns. Clades show considerable phylogenetic momentum with species strongly constrained by both environment and distance. Species from disparate clades have dispersed beyond Africa with records from Madagascar, Cape Verde, and Yemen, as well as central America and Australia. Analysis of species distributions in conjunction with environmental envelopes points towards additional evidence for an "arid track"? Importantly unlike most Cape Clades, *Hermannia* species tend to occupy the nutrient rich lowlands. This has had profound impacts on the evolution of the group and the resulting pattern of species distribution. Analysis of distributions reveal several regions of high turnover and endemism. Species composition points towards regions that are closely allied to that of biomes, showing that *Hermannia* has species patterns that are broadly representative of vegetation types. This makes the genus a strong candidate for a future public atlas like that of the Protea Atlas and highly complementary to that of the Proteaceae in that the genus is distributed far beyond the narrowly confined distribution of the Proteaceae.

Keywords: biogeography, dispersal, distributions, vegetation types

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*Speaker

Biological Invasions on Islands

Contents

Predicting future invasive non-native species across UK overseas territories – global information effecting changes at a local level

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Invasive non-native species (INNS) are one of the major drivers of change that can negatively affect biodiversity, ecosystem services and human health; islands are particularly vulnerable to biological invasions. Horizon scanning can be used to prioritise and rank INNS yet to arrive in a location, in order to inform decision-making and action, with scale and scope varying depending on the need. Biosecurity is a series of measures to protect against the entry and spread of INNS. The UK has 16 Overseas Territories (UKOTs), many of which are islands. We undertook horizon scanning using consensus methods for each of the UKOTs and linked the outcomes through a workshop to consider approaches for enhancing biosecurity. Funded through the GB Non-Native Species Secretariat by the UK Government, a team of ecologists led by the Centre for Ecology and Hydrology worked with regional experts to derive a list of invasive non-native species with the potential to arrive, establish and threaten biodiversity and ecosystems, human health or the economy. The derived lists of species were used to develop Pathway Action Plans (PAPs) in collaboration with the regional experts and guided by the biosecurity teams. Pathway Action Plans identify the most likely pathways of arrival for a species and then develop pathway based mitigation to reduce the risk of arrival of that species. The lists have been embedded within conservation action plans for some of the UKOTS. These workshops have demonstrated the excellent applicability of these methods to effect on the ground changes and support biosecurity guidance. Combining the horizon scanning consensus approaches with biosecurity pathway action planning has demonstrable impact for improved knowledge exchange, support and network development and could be effective across other island states.

Keywords: invasive non native species, biodiversity, ecosystem services, human health, UK Overseas Territories

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Colonization and dispersal rate of two Trichoptera species in Iceland and the consequent exclusion of a Trichoptera species

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During the 20th and 21st century two species of caddisflies (Trichoptera) have colonized Iceland. One species is *Potamophylax cingulatus* and the other is *Micropterna lateralis*. *Potamophylax cingulatus* is widely distributed in streams in Europe and is dominant at higher latitudes and elevations. The larvae feed on detritus in the streams and to some extent on invertebrates. In Iceland, it is a predator of the Holarctic caddisfly larvae *Apatania zonella*, which has become extinct in streams recently colonized by *P. cingulatus*, probably due to predation. *P. cingulatus* was not found in several extensive surveys before WWII, conducted by several entomologists and published in 1942. During a survey in streams in 1974 – 1978 the species was found to be common in eastern and north-eastern part of Iceland, but the Trichoptera species *A. zonella* was absent from the same streams, where it was common before WWIIl. Searching earlier collections of unidentified Trichoptera, a single specimen was found in East Iceland in 30 July 1959. The survey was repeated in 2006, and the species had colonized most streams and rivers in Iceland, and *A. zonella* has disappeared from most of them. *M. lateralis* was found in a single light trap near Reykjavik in 2004 - 2008. The annual catch has since grown from 2 specimens to 73, but the species has not been found elsewhere and the larvae have not been found, but they are supposed to occur in running waters. It is possible to conclude from this that when species establish a population on a large island like Iceland, the population builds up and when it has established itself, it disperses fast. For *P. cingulatus*, the dispersal rate was about 7 km/year, but the dispersal rate for the more recent settler *M. lateralis* has to be seen.

Keywords: Trichoptera, colonization, dispersal, species exclusion, population growth

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History and impacts of the introduced smooth-billed ani *Crotophaga ani* in Galápagos

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Smooth-billed anis *Crotophaga ani* were introduced to Galápagos in the 1960's, reportedly by farmers hoping they would eat the ticks off their cattle. Since then, this bird species has spread around most of the archipelago and reached an estimated population of 250,000. They are considered by many to be a damaging invasive and are possibly impacting upon native species and ecosystems via multiple mechanisms. However, evidence for this is largely anecdotal and research on smooth-billed anis in Galápagos is limited. Despite this, there have been repeated attempts to control or eradicate the population over the past few decades, all without long-term success. These attempts continue, but no official plan of action regarding this species currently exists. In attempt to improve knowledge of this species, we completed a full review on all available published and unpublished research on smooth-billed anis in Galápagos. In addition, we designed and successfully tested a new trap to catch anis and performed a dietary analysis on 119 birds. We highlighted numerous knowledge gaps in both the current understanding of the impacts of this introduced species and the effectiveness of potential control or eradication methods. We also reported previously unknown examples of depredation by smooth-billed anis on both endemic species and other introduced species, the latter of which it may be helping to control. We find an urgent need for further research before considered, resource-efficient decisions can be made regarding smooth-billed anis in Galápagos. We also note the importance of accounting for impacts on other introduced populations, if widespread smooth-billed ani control is to be attempted.

Keywords: invasive species, alien bird species, island invasions, introduced species impacts, control

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Alien species on tourists' cloths as novel threats for island floras: Human-dispersed seeds survive and can disperse after laundry washing

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Due to increased human mobility, cloth-dispersed seeds can be transported over long distances, which would not been bridged otherwise. Thus, human-mediated seed dispersal is an important threat for the flora of islands. We studied a formerly overlooked component of human-mediated plant dispersal by assessing the effects of laundry washing on the dispersed seeds. We asked the following questions: (i) Are cloth-dispersed seeds able to germinate after the laundry cycle? (ii) What are the effects of washing on the fitness of germinated seedlings and on the temporal dynamics of germination? We studied the germination of 18 species (families: Poaceae, Rosaceae, Asteraceae, Rubiaceae, Apiaceae), which have morphological adaptations for epizoochory and are commonly dispersed by people. We tested five replicates of 25 seeds per treatment, i.e. 875 seeds per species and a total of 15.750 seeds. We tested six treatments (washing with water, washnut or detergent, at 30∘C or 60∘C) compared to an untreated control. We also measured the seed retention rates of dry and washed seeds on three cloth types (fleece sweater, blue jeans, cotton socks). Our results showed that washing temperature was the most significant factor affecting germination. Washing at 30∘C did not suppress germination of any of the studied species. Washing at 60∘C supported the germination of two species, but suppressed six species. The intensive washing treatments at 60∘C decreased significantly the synchrony of germination. Our measurements showed that more than 70% of attached seeds remain on our clothes for more than 8 hours and have the chance to enter the laundry cycle. 64% of washed seeds fall down from clothes during drying. The remaining 36% of washed seeds can further disperse over a longer distance. Several factors influence seedling establishment after washing, icluding potential mechanical effects (removal of seeds, ironing) and the availability of suitable habitats; however our study shows an important pathway for the introduction of non-native and viable seeds to islands. We showed that people are not purely transporting seeds from one location to another, but via the laundry cycle we also influence the fate of the transported seeds by affecting germination potential and dynamics.

Keywords: human mediated seed dispersal, long distance dispersal, invasive plant, seed germination, seedling establishment, invasion risk

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Rapid assessment of plant invasions in natural and semi-natural forest habitats in Grande Comore island

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Comoros archipelago is a biodiversity *hot spot* characterized by a relatively dynamic land use change. Natural forests in these islands are exposed to serious anthropogenic-induced threats with severe impacts on the structure of biodiversity. Among these, biological invasions by exotic plants remain a serious problem that hinders the conservation of native vegetation in Comoros. It is therefore necessary to establish management priorities for these forest remnants, but reference data barely exists on the invasion level of forest habitats by plants in the archipelago. In this study, we focus on the island of Grande Comore and specifically address the two following questions: (*i*) which plant species are the most invasive and (*ii*) what are the invasion level of different forest habitats? This study has been conducted on exotic woody plants. Surveys were targeted at lowland and sub-mountain forests on 44 transects of 150 X 10 m from 23 to 1047 asl. Transects were divided in sections of 30 m to facilitate the recording of species invasion levels, habitat types and land use. Sampling was carried out on individuals whose size was superior to 1 m. Major invasive plants in natural and semi-natural forests include *Psidium cattleianum*, *Clidemia hirta*, *Furcraea foetida, Rubus rosifolius* and *Syzygium jambos.* In term of habitats, lowland forests have been cleared and replaced by plantations (coconut and / or fruit trees). The sub-montain forests dominated by native species of *Nuxia*, *Ocotea* and *Tambourissa* are typically uninvaded in their canopy whereas sub-mountain forests dominated by *Weinmannia* is invaded in the understory and the canopy. The results obtained represent the first assessment of plant invasion in forests on Grande Comore. In order to define management priorities, it is necessary to expand these surveys. Results of this study will contribute to improve decision-making for the National Park program in Comoros.

Keywords: exotic woody plants, Madagascar and Indian Ocean biodiversity hot spot, forest habitat, anthropogenic disturbances, island conservation

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Deciphering the invasive history of a bacterial crop pathogen in the Southern Indian Ocean islands: insights from historical herbarium specimens

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Crop pathogens have been a threat to human kind since the birth of agriculture. However, little is known on the evolutionary processes and ecological factors that underlie their emergence and success, and explain epidemics. Insular ecosystems are especially vulnerable to exotic disease invasions and thus provide a model of particular interest. Nowadays, our understanding of plant pathogens and the diseases they cause greatly benefits from molecular genetics and genomics. In this context, herbarium collections are an enormous source of dated, identified and preserved DNA material that can be used in comparative genomic and phylogeographic studies to elucidate the emergence and evolutionary history of pathogens. In this study, we reconstructed the genomes of 6 historical strains of the Citrus phytopathogen *Xanthomonas citri* pv. *citri (Xcc)* obtained from infected herbarium specimens. We designed a specific extraction protocol suited for bacterial ancient DNA (aDNA) from herbarium specimens, and showed the authenticity of our historical samples by assessing DNA damage patterns. We then compared the historical strains to a large set of modern genomes to reconstruct their phylogenetic relationship and estimate several evolutionary parameters at the scale of the Southern Indian Ocean (SIO) islands, using Bayesian tip-calibration inferences. Our results first confirm that *Xcc* originated in Asia and subsequently spread to the rest of the world, including the SIO islands. We dated the arrival of *Xcc* in the SIO area to the mid-19th century and hypothesize that it was linked to human migrations following the abolishment of slavery. By analysing the phylogenetic structure of SIO *Xcc* we suggest that the introduction of the disease happened first in La Réunion and Mauritius, from which it spread to all other SIO islands. Finally, our results also include the first estimation of a mutation rate for a plant pathogenic bacterium. Our study shows the great potential hidden in herbarium collections to bring light on the evolutionary dynamics that drive pathogens invasion at the scale of the Southern Indian Ocean islands, ultimately helping us to better control current and future crop epidemics.

Keywords: island phylogeography, ancient DNA, population genomics, invasive species, Southern Indian Ocean islands

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Bioscecurity challenges and progress at the UNESCO site of Aldabra atoll, Seychelles

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Invasive alien species (IAS) are widely recognised as a major threat to biodiversity and their impacts on native species and whole ecosystems can be devastating. This is particularly true for islands, which hold a high proportion of unique species and ecosystems. Prevention of IAS incursion requires far fewer resources than responding to an IAS incursion or eradication. Furthermore, the chances of successful interception of IAS are higher before they arrive on an island. Consequently, it is essential for islands to have thorough IAS prevention and detection procedures in place, as well as robust emergency response measures, to minimise the risk of IAS establishment and subsequent need for eradication. Aldabra Atoll (154 km2), a UNESCO World Heritage Site in the Seychelles, is a remote, universally outstanding example of a coral atoll and refuge for a range of threatened and unique species, with only a small research station staffed by 15 people. Since 2012, biosecurity practices have been developed for Aldabra which are now in the final stages of implementation. Aldabra's biosecurity strategy focuses on prevention and early detection, which required significant investments into capacity and infrastructure development. Specific actions include risk assessments for potential IAS, ensuring pest-free quarantine facilities and transport to Aldabra, controlling IAS pathways, mainstreaming of biosecurity practices, conducting regular IAS surveillance monitoring and being prepared to respond rapidly to a range of IAS incursions. Substantial investment (€ 140,000) was made into quarantine facilities and institutional capacity building with dedicated biosecurity officers now in place for both sites. These measures, combined with early detection and surveillance training for all staff, are essential to prevent IAS from reaching Aldabra, and have greatly reduced the chances of introduction of new IAS on Aldabra. Since strengthening biosecurity in 2017, no potential IAS has been intercepted on Aldabra, compared to four separate interceptions during the previous 4 years. Biosecurity capabilities could be further developed with other island nations across the region, and cooperation between nations and organisations strengthened to better protect Indian Ocean islands with high conservation value.

Keywords: biosecurity infrastructure, invasive alien species (IAS), island biodiversity, risk assessment, surveillance

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[*] Speaker

Quantify invasion levels by alien plant species in La Réunion Island

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The largest area of intact vegetation in the Mascarene Archipelago is found on La Réunion Island. In 2007, a national park has been established where most protected habitats and rare species are targeted by some conservation actions. Invasions by exotic plants are the main threat to the biodiversity within this park and several management programs aim at controlling the main invasive alien plant species. For decades, inventories of alien species have been carrying out at La Réunion, constituting a large amount of data but these data never been synthetized, assembled and exploited to assess the level of invasion. Here, data from different organizations were combined to quantify the overall level of invasion by exotic plants island-wide. These data were extrapolated to grid cells of 250 x 250 m and categorized into four invasion categories ranging from intact to heavily invaded areas. Here, we present the spatial pattern of invasion on La Réunion Island. Only 12% of the island remain intact while 60% is moderately to heavily invaded. Inside the national park, more than 55% is lightly invaded or intact. We then discuss the invasion rate according to several factors: altitude, habitats, geomorphology, land cover and the presence of pathways or streams.

Keywords: La Réunion Island, invasive alien plants, mapping, spatial ecology, determinants of plant invasions

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Coordinating the fight against invasive alien species: 8 years of operational planning in Reunion Island

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Invasive alien species (IAS) are acknowledged as one of the major causes of biodiversity loss worldwide, especially in oceanic islands. In Reunion Island, pristine natural habitats cover 30% of the territory, the largest area of intact habitats in the Mascarene Archipelago. To ensure the protection of these habitats and rare species, a national park was establised in 2007, protecting 42% of the island's area, and has since been included on UNESCO's 2010 World Heritage List. To tackle biological invasions, an IAS Strategy was developed in Reunion Island in 2010 and implemented in two Operational Control Plans for Invasive Species (2010-2013 and 2014-2017). Here, we used semi-structured interviews, SWOT analyses, workshops and all relevant data and references about biological invasions in Reunion Island to assess the efficiency of these plans. Costs over 8 years amounted to € 20 million and were mainly allocated to control the expansion of IAS. We identified the most important invasive species in terrestrial biomes and developed an online public detection platform to enable prompt, practical responses to new invasions on the island. Hence, early detection of the house crow (*Corvus splendens*) and the African herb dream (*Entada rheedii*) have allowed their eradication. The efforts of various stakeholders (public institutions, research organizations, universities, associations) is at the heart of the control of IAS in Reunion Island. The diversity of stakeholders allowed work to take place simultaneously on several fronts. Despite significant spending for the island and a strong local effort, biological invasions appear to have increased in many protected areas, causing UNESCO World

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Heritage to drop their conservation status for the island in 2017. Our findings suggest that the IAS Strategy in Reunion Island should be substantially modified if impacts are to be effectively mitigated. Rather than attempting to operate on all species and in all areas, prioritizing both species and areas and setting goals and monitoring their effectiveness through indicators within a framework of adaptive management is essential. Strengthening regulation to prohibit entry of new species is necessary. A greater proportion of human and financial resources should also be allocated to the control against IAS.

Keywords: invasive alien species, Reunion Island, strategy, control, operational planning

Interspecific interactions between a new invasive Tephritid fruit fly, *Bactrocera dorsalis*, and other resident species in an insular context

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The impact of biological invasions of insects considered as pests have important negative impacts on the economy and the environment, particularly in insular ecosystems. Since the detection of one of the most harmful pest of fruit and vegetable crops, *Bactrocera dorsalis*, in April 2017, La Réunion counts nowadays nine pests species of Tephritid fruit flies of economic importance. A biological control agent, the braconid wasp*, Fopius arisanus*, was initially introduced in La Réunion in 2003 to control another fruit fly of the same genus: the peach fruit fly, *Bactrocera zonata. Bactrocera dorsalis,* in its native area is the main host of this braconid wasp and will probably be able to parasitize it in La Réunion. To understand the invasion process of *B. dorsalis* and the impact of this new introduced fruit fly on the community structure of the resident Tephritid species, and the parasitoid, *F. arisanus*, it is necessary to study the competition interactions. We first assessed the interspecific competition between *Bactrocera dorsalis* and four other fruit flies, *Bactrocera zonata, C. capitata*, *C. quilicii* and *Ceratitis catoirii.* Three of those fruit flies are successive invaders in La Réunion and one endemic species. We focused our study on the interference competition among pairs of adults, measuring the ability of a female to remove another one from a fruit for the laying behavior in controlled environments.The parasitoid preference for both sympatry species of genius Bactrocera were observed. On one hand, we observed the preference for eggs only and on the other hand, the preference for one particular species according to the host fruit in choice experiments.

Keywords: Biological invasion, Bactrocera dorsalis, Fopius arisanus, interference competition, indirect interactions.

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Remoteness promotes the biological invasions on islands worldwide

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Islands are hotspots of alien species invasions, and their distinct biodiversity is particularly vulnerable to invading species. While isolation has shaped natural colonization of islands for millions of years, globalization in trade and transport has led to a breakdown of biogeographical barriers and subsequent colonization of islands by alien species. Using a large dataset of 257 subtropical and tropical islands, we show that alien richness increases with increasing isolation of islands. Interestingly, this pattern opposes the well-known negative SIR of native species and is consistent across four taxonomic groups (plants, ants, mammals, and reptiles). We argue, that alien species richness on islands cannot simply be explained by island economics and trade alone but that the reversal of the SIR for alien species is driven by an increase in island invasibility due to reduced diversity and increased ecological naiveté of native biota on the more remote islands. Hence, geographical isolation does not protect islands from alien species, and island species richness may reach a new dynamic equilibrium at some point, likely at the expense of many endemic species.

Keywords: isolation, island invasibility, naturalization, plants, birds, mammals, reptiles, ants

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[*] Speaker

The invasion of the Lime Swallowtail in Australasia and its effect on endemic populations in the Lesser Sunda islands

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The original range of the Lime Swallowtail (*Papilio demoleus* L.) consisted of two parts: (1) continental South and SE Asia, including the islands of Sri Lanka, Hainan and Taiwan; and (2) Australia (ssp. *sthenelus*), SE Papua New Guinea (ssp. *novoguineensis*), and the Lesser Sunda Islands (ssp. *sthenelinus*). Populations in the Australian region are well differentiated genetically from Asian ones, in adult phenotype, larval colour pattern and foodplant choice. Whereas larvae of Asian populations are a pest on *Citrus* (Rutaceae), those in the Australian region only feed on *Cullen* (Fabaceae). Since the 1950s, *Citrus* feeding populations have invaded most of the previous distributional gap, starting from the Phillippines through the Greater Sunda Islands, and also reaching the Lesser Sunda Islands (Flores in 1997) and Papua New Guinea (in 2004) with their indigenous *Cullen* feeding populations. Molecular analyses of mitochondrial DNA (*COI* & *COII*) prove that the indigenous populations in PNG and Flores are well differentiated genetically from invasive ones and closely related to Australian populations while all invasive populations are very similar genetically and originate from Southeast Asia. The most common *COI* haplotype which spread across most SE Asian islands and which was also introduced into the Caribbean originates from the SE Asian mainland or Hainan (China), a second haplotype spread from Taiwan via the Philippines to the Lesser Sunda Islands, and a third haplotype with as yet unknown origin was only found in Sumatra, the Lesser Sunda Islands and West Papua. Despite the invasion into the Lesser Sunda Islands, indigenous populations still exist on the west coast of Flores and the nearby islands of Komodo, Rinca and Padar, where they feed on the endemic *Cullen gaudichaudianum*. Whereas no evidence of mitochondrial introgression was found at Labuanbajo, where indigenous and invasive populations occur in sympatry, genetical admixture could be established at the nuclear locus *ef-1*α. Nevertheless we suspect that the taxon *sthenelinus* constitutes a distinct species, but further studies are needed to clarify the taxonomy of the *Papilio demoleus* complex and the extent of gene flow between indigenous and invasive populations, which might pose a threat to the endemic island taxa.

Keywords: invasion biology, phylogeography, hybridization, introgression, conservation, life history traits, Lepidoptera, butterflies, Indonesia, Lesser Sunda Islands

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Population dynamics and damages of the invasive phloem-feeder psyllid *Acizzia uncatoides* (Hemiptera : Psyllidae) on the endemic tree *Acacia heterophylla* on La Réunion Island

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Phloem feeders, such as psyllids, are known as pests in agriculture and in natural ecosystems. *Acizzia uncatoides* (Ferris & Klyver, 1932), originating from Australia, is an invasive psyllid pest on *Acacia koa* in Hawaii. On la Réunion Island, this psyllid species has been found on *Acacia heterophylla* Willd since 2010 and formally identified in 2016. This endemic tree is the dominant canopy tree in Acacia mountain forests, distributed throughout the National Park of the territory. In this study, population dynamics and the impacts of the psyllid on *Acacia heterophylla* were studied. A survey was conducted by monitoring four altitudinal transects set up within the National Park between 1350 to 2350 m from Jan 2017 to Jan 2019 on a monthly basis. Damages on *Acacia heterophylla* were recorded in terms of defoliation and tree mortality on 713 individuals within six 250 m2 plots. Populations of *Acizzia uncatoides* were assessed by 1-min suction sampling with a leaf blower vac covered with mesh fabric bags. The higher the elevation is, the more numerous and damaging the psyllid appeared to be. *Acizzia uncatoides* was found in all transects in the 11 sites throughout the year with a population peak in October-January. We found up to 60,000 adults in 1-min mechanical aspiration at 2350 m. Defoliation was severe in 5 sites and up to 30 % tree mortality was observed in 250 m2 quadrats. The risks to endemic forests of Reunion Island and the possibilities of biological control of *Acacia uncatoides* are discussed.

Keywords: Acizzia uncatoides, Acacia heterophylla, invasive psyllid pest, threatened native species, population dynamics

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Feral cat threat on French Polynesia inhabited islands: influence of island characteristics

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Invasive populations of feral cats strongly threaten the native fauna on islands worldwide. French Polynesia, formed by five archipelagoes located in the South Pacific, is included within the 36 global biodiversity hotspots and harbors several threatened endemic species. Feral cats were introduced by European settlers 200yrs BP and are currently present in most habitats of many islands, but their abundance and impacts remain largely understudied compared to other invasive mammalian predators such as rats. The French Polynesian islands are multi-invaded systems and show various assemblages of introduced rodents. The impact of feral cat populations is assumed to be higher in presence of introduced rodents and may also vary according to the rodent species. In particular, black rats *Rattus rattus*, which constitute a constant and abundant resource, can help sustain feral cat abundance at a high level, thereby exacerbating predation pressure on native wildlife via the "hyperpredation" process. Here, we investigated the feral cat's impact on four contrasted inhabited tropical islands, particularly in terms of introduced rat species: two islands in the Marquesas - Ua Huka (free of black rat and brown rat *R. norvegicus*) and Tahuata (free of brown rat) - and two islands of The Society: Moorea and Tahiti (harboring black, brown and Polynesian rats *R. exulans*). We studied cat diet by trophic analyses using feral cat scats sampled from these four islands across 2 surveys (2018-2019). Cat abundance was estimated using baited camera traps as "capture" method, giving an abundance index for a mean effort of 299.3±48.3 camera-trap days over 15 days between June and September 2018. Our study reveals previously unreported patterns of cat relative abundance; in the Marquesas islands, we obtained 2.1 detections/100 camera trap-days for Ua Huka and 0.5 detections/100 camera trap-days for Tahuata. In the Society islands, we obtained 0.03 and 0 detections/100 camera trap-days for Moorea and Tahiti respectively. Camera-trapping was confirmed as a useful tool to survey feral cats in tropical forest habitats, in order to inform future management decisions and priorization, especially on data-deficient islands requiring studies of feral cat impact.

Keywords: birds, camera trap monitoring, diet, endemic species, Felis catus, invasive predator

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What are the possibilities of *Halicarcinus planatus*, a subantarctic crab, to survive in the West Antarctic Peninsula?

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In the last 50 years, anthropogenic activity and atmospheric temperature in the West Antarctic Peninsula have increased and consequently facilitated the establishment of exotic species. In 2015, a 2010 discovery was reported of an ovigerous female of *Halicarcinus planatus* in shallow waters of Deception Island. *Halicarcinus planatus*, is a small brachyuran crab distributed in southern South-America and the Subantarctic islands, with a planktonic larval phase of 45 to 60 days. Moreover, *H. planatus* has the ability to down-regulate haemolymph's magnesium ion concentration ([Mg2+]) below seawater concentration, that would help to survive in shallow cold waters. The present study evaluates the physiological ability of *Halicarcinus planatus* to establish in current and projected future abiotic conditions in the West Antarctic Peninsula, in order to make predictions on the establishment of *Halicarcinus planatus*. In order to evaluate if this species is able to survive winter conditions in the Antarctic waters, a survival experiment was realized with *H. planatus* adults at different temperatures (-1.5, -1, 0, 1, 2 and 5◦C) for 90 days by determining survival, mobility and quantify metabolites. In parallel, we established an "Ecological niche" of *Halicarcinus planatus*, gathering all available data on the crab occurrence, from geo-referenced sampling site to bibliographic records. Then, we calculated the maps of current and future spatial predictions. We based us on relevant factors for the specie as current and future temperature. The mortality at -1.5, -1 and 0◦C reached 100% at day 11, 15 and 59 respectively, whereas at 1, 2 and 5◦C, the mortality dropped at 40%, 25% and 5% respectively, at day 90. The haemolymph analyses at different temperature indicate that this species regulates the [Mg2+] above 1◦C; indeed below 0◦C, the concentration increases significantly. Our results indicate that this crab could survive in the Antarctic Peninsula only in summer, when seawater is over 1◦C and will not survive to current winter conditions at seawater temperature below 0◦C. However, if seawater temperature increases enough and it is not freeze in winter, *Halicarcinus planatus* could arrive and install in the West Antarctic Peninsula.

Keywords: climate change, crab, physiology, sub Antarctic

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Putting the green light on native island species – the help of negative legislative lists

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Invasive species still represent the dominant and most pervasive threat associated with native species extinctions on islands. Recently, many legislative changes were carried out by the European Union to tackle the introduction and spread of invasive species. One of the main achievements is the invasive union list, which is an inventory of the most worrying invasive species requiring priority management. These legislative changes are very recent and encouraging, but time is running out and a more efficient regulatory tool is required to curb species introduction worldwide. We made a global review of the main recent changes in European and French legislations that aim to limit the introduction and/or spread of invasive species on insular territories, and compared them with legislations from other countries facing similar issues (e.g. Australia and New Zealand). Additionally, we evaluated the effect of green lists, which are already used in ornamental plant trade, to question the effectiveness of negative lists, used for preventing new introductions and limiting the spread of invasive species. Our results show that negative lists (i) represent promising solutions to prevent new introductions on islands and to avoid the costly management of introduced species, (ii) are also positive and more easily accepted by people because they list native species that can be spread in the targeted islands, (iii) are easier to use and to apply as they are exhaustive, and (iv) may help manage previously introduced invasive species as they provide a complete list of native species.

Keywords: green lists, invasive species management, legislative tools, preventing introductions, positive management

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Characterization of the skin and gut bacteria communities of the invasive Asian Toad in Madagascar and comparison with a native species

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Biological invasions have emerged as one of the primary sources of global biodiversity loss, with climate changes, habitat alterations and anthropogenic influence being among the main factors facilitating their worldwide spread. Biological invasions can pose multiple threats to native species through competition for natural resources, predation or transmission of diseases, among others. The success of invasive species has been attributed to habitat plasticity, high reproduction rates or generalist life traits. The microbiota community of invasive species can also have an important role in this process, and understand how this community, and its functions, changes in an invasion scenario can provide useful information on the host resilience and adaptability to new habitats. The invasive *Duttaphrynus melanostictus* has recently established in Madagascar and it now poses several threats to the native ecosystems. We characterized the skin and gut bacterial communities of the invasive toad population in Tamatave (Eastern Madagascar) and we compared these communities with the ones of a co-occurring native frog species (*Ptychadena mascareninesis*) across three sites within the incursion range of the toad. We identified significant differences between the two amphibians and found that the toad carries a richer and more diverse skin and gut communities. At lower microbiota taxonomic levels, the differences are more incisive and may reflect effects of host behaviour, microhabitat and diet preferences. Our study provides the first characterization of both skin and gut microbiome on one invasive and on a native co-occurring species.

Keywords: 16S rRNA gene sequencing, bacteria community, Eastern Madagascar, invasive species, species interaction

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Insect herbivory on native and alien plants in Iceland

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Insect herbivory dynamics are changing in high latitudes, including in islands like Iceland. Several Icelandic moths such as the red-backed cutworm (Euxoa ochrogaster), broom moth (Melanchra pisi), and satyr pug (Eupithecia satyrata) have shown host expansion to Nootka lupine (Lupinus nootkatensis), an invasive plant native to North America. The broom moth and satyr pug can cause damage to various tree species, while the red-backed cutworm can be a horticultural pest. However, there is limited knowledge on their interactions with native and alien plants in Iceland. Given this data gap, I began in 2015 a study to assess the distribution and herbivory in southern Iceland of the red-backed cutworm, broom moth and satyr pug on Nootka lupine and horticultural crops (alien plants, n=12 sites) and lyme grass (native plant, Leymus arenarius, n=6 sites). Larval surveys were conducted in June (red-backed cutworm) and August (broom moth and satyr pug) by checking individual plants for herbivory and larvae for 20 minutes. Moreover, a 50-m transect line with randomly placed 0.25 m2 quadrats was used to further assess plant cover and larval abundance of the red-backed cutworm. Adult surveys occurred in August for the red-backed cutworm using pheromone traps that attract male adults. Results indicate that from 2015-2017 the larval abundance of red-backed cutworms ranged from 0-31 larvae/site. Sites with Nootka lupine had the highest larval abundance, but it was not significantly greater than in sites with lyme grass. The abundance of male adults of red-backed cutworm, varied greatly among years regardless of host plant. Overall, 65 males/site were found in 2015, whereas in 2016 and 2017 less than 1 male/site. Red-backed cutworm herbivory on alien plants included Nootka lupine, rutabagas (Brassica napobrassica), and carrots (Daucus carota). Herbivory was also found on five native plants including lyme grass. Broom moth herbivory occurred on alien plants such as Nootka lupine, rutabagas, rapeseed (B. napus), carrots, and on at least seven native plants. Broom moth herbivory on horticultural crops are new host records. These results highlight the importance of long-term monitoring to assess herbivory dynamics of native insects and their interactions with agricultural systems.

Keywords: agriculture, insect herbivory, native plants

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Ecological Characterization of the vegetation of *Ravenala madagascariensis* and *Sticherus flagellaris* invasive species in Betampona Nature Reserve

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Invasive species and harmful native species is one of the threats to the Betampona Natural Reserve. Ravenala madagascariensis and Sticherus flagellaris are native species but have harmful effects on forest regeneration in the Reserve. The objective of this study is to investigate the formations of Ravenala madagascariensis and Sticherus flagellaris and to know their distribution with two other invasive species (Aframomum angustifolium and Rubus moluccanus). The linear method of Gautier and Braun Blanquet's quadrat method was used for the ecological characterization. Multivariate analysis shows three floristic groups of Ravenala madagascariensis and Sticherus flagellaris are obtained according to abundance. In the Betampona Reserve, it is essential to control these problematic native and invasive species to properly conserve the biodiversity of the Reserve.

Keywords: Invasive species, floristic groups, Madagascar, Nature Reserve

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Ecological characterization and evaluation of the production of *Ravenala madagascariensis* Sonn. in the savoka of East Ranomafana and its surroundings (Brickaville district)

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Ravenala madagascariensis (Streliziaceae), commonly referred to as the "Traveler's tree", is an endemic plant to Madagascar well known by the fan arrangement of its leaves. Furthermore, this plant is considered to be an invasive natural species of open environment of the eastern facade of the abundant precipitation in such environment. Although this sector is very meaningful and sought for its various uses especially in terms of building and medicine, it remains at the level of traditional uses. Providing ecological knowledge on these species and promoting the conservation and rational exploitation of this resource are the main objectives of this project. Yet, it is also considered as an orientation on the sustainable management of the biological resource of our country. In this respect, nine ecological types have been studied, divided into three types of formation which constitute the main objectives, of this project as well such as: Bemavo a variety of formation, formed for both varieties or the transition zone and formation in Horonorona. These two types of Ravenala madagascariensis are chosen for their abundance and multiplication that are amazingly faster. The biogeographic distribution of both varieties also varies depending on topographic and soil substrates. Frequently found from 300 to 500 m altitude, in the high slopes, soils drained with silty texture, the Bemavo variety is really unique. Whereas the variety Horonorona prefers the low-area which pours down to the bottom in a hydromorphic soils loamorly texture. As far as natural regeneration is concerned, the multiplication of the Horonorona variety is the fastest with a regeneration rate of 981 percent. *Ravenala madagascariensis'* leaves cannot be harvested until after eight months of cutting while monitoring natural regeneration. Finally, the Horonorona variety is the most profitable in terms of dry leaf biomass production due to its very large surface area and its very high density of 183 species per hectare. In addition, invasive plant species are strongly desired to be valued in Madagascar, specially the case of *Ravenala madagascariens.*

Keywords: Brickaville, ecology, Madagascar, natural regeneration, Ravenala madagascariensis, savoka

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*Speaker

Distribution of the invasive species *Nicotiana glauca* R.C. Graham on recent lava fields. Evaluation of the degree of invasion and proposals for control

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The European Council Directive on the conservation of natural habitats, wild fauna and flora includes the Habitat 8320, Lava fields. These habitats are present in the Canary Islands, mainly in the eastern islands, Lanzarote and Fuerteventura. In recent years there has been an increase in the naturalization of exotic flora, which is quite worrying especially when it affects habitats in which invasive species can behave as early colonizers. This is the case of Habitat 8320, characterized by the presence of very specific native communities or by the absence of vegetation, with abundant lichen communities. We aim to characterize the invasion of these habitats and propose measures of eradication. Nicotiana glauca is an invasive in the Canaries that forms monodominant populations competing with native species in these habitats, limiting their growth and inhibiting their germination, with the leaching of their leaves and twigs. This species is capable of displacing endemic species and altering ecological conditions such as light, nutrients and the availability of water and substrate, especially in habitats as sensitives as recent lava fields, while it also promotes the arrival of other potentially invasive species. We implemented a Geographical Information System georeferencing of grids occupied by lava fields at a 500 x 500-meter resolution and incorporating a database on the abundance, phenology, vitality status and age structure of the species and the accompanying endemic and invasive plant species. The cartography and spatial analysis along with the database of attributes, and the incorporation of data on the occurrence of other invasive plants allows us to establish which areas should be prioritized for control and the general state of conservation of the habitat. The proposed control and eradication measures are based on: 1) physical methods, consisting of pulling the plant out by hand or with tools, including both seedlings and young plants, 2) chemical methods, based on cutting large individuals and treating the stumps with herbicide in those areas where this treatment does not affect other elements of the habitat, and 3) biological methods, already tested in other invaded areas, spraying the plants with herbicide and exposing them to parasitic Coleoptera.

Keywords: control and eradication measures, invasive species, recent lava fields, spatial analysis

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*Speaker

Community / Functional Ecology

Contents

An analysis of global trait spaces of birds on islands

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The equilibrium theory of island biogeography (ETIB) predicts island species richness patterns based on immigration and extinction processes, which are influenced by island characteristics, namely island isolation and area. Recently, the rise of trait-based approaches has influenced the field of biogeography, including the ETIB. For example, dispersal and resource-acquisition traits should influence species likelihood of species to reach and to colonize islands. Here, we present an analytical framework (along with preliminary results) that integrates various traits in a multi-dimensional trait space and links them to the predictions of ETIB, using the bird communities of the world's islands as a study system. We hypothesize that island isolation and area influence the structure and size of the trait space of island bird communities. Specifically, island isolation should influence colonization whereas island area should affect the trophic structure of the island communities. We thus expect that (a) the occurrence of species on isolated islands is mainly limited by dispersal traits (measured e.g. by morphological traits such as wing characteristics or body size), and that (b) the occurrence of species on small islands is mainly limited to species from low trophic levels, such as frugivores and herbivores. Eco-morphological traits as surrogates for resource acquisition and dispersal characteristics will be obtained from museum specimen and public databases as well as from the literature. Information on species distribution data and on geophysical island characteristics will be compiled from published databases as well. The data are analysed using multivariate regression and ordination techniques, in a spatial context and accounting for potentially confounding factors such as climatic conditions, elevation, age and geological origin. The results of the analytical framework presented here provide general insights into the determinants of the variation of trait spaces among different island bird communities and thus to a better understanding of the variation of functional diversity on islands in general.

Keywords: birds, community ecology, traits, dispersal, trophic structure

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Intraspecific variability of functional and chemical leaf traits of the endemic *Acacia heterophylla* along three elevational soil gradients in Réunion island (Mascarenes)

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*Acacia heterophylla*is an endemic tree structuring the tropical montane cloud forests of La Réunion, present along a large elevation profile (900 to 2400 m) from the wet-East to the dryer-West side of the island. Does the species modify its nutrient allocation strategies to live under these variable climatic and edaphic conditions? Could intraspecific variability of leaf functional and chemical traits reveal potential strategies along environmental gradients? To answer these questions, we sampled 86 adult trees in 14 sites, along three transects under different climate conditions (East, West and South) between 1250 and 2350 m a.s.l. We measured functional leaf traits related to resource-use strategies (SLA, LDMC), foliar nutrient content (N, P, Ca, K, Mg), carbon and nitrogen isotopic composition (foliar δ13C, δ15N), and tree morphology (height, diameter). Chemical profiling was investigated, using 1H NMR-based metabolomics approach. We also described humus form, as a proxy of soil nutrient conditions. For both polar and apolar leaf compounds, multivariate analysis of the1H NMR data show intra-specific variability of chemicals produced by *A. heterophylla*among the three elevational transects. Elevational influence was significant for trees living in the cloud forest ($>$ 2100 m): smaller height and SLA indicated a more conservative nutrition strategy, but also dryer conditions (higher δ13C values). At lower elevation ($<$ 2100 m), *Acacia* shows greater foliar δ15N and occurrence of nitrogen fixing root nodules in the East, where humus forms show a slower litter decomposition rate (*mor* forms) under acidic conditions (pH 4). However, N and P content and SLA are similar compared to other transects. This seems to indicate some efficient compensation mechanisms in the root environment (nodules, mycorrhiza), leading to a greater plasticity in nutrient allocation strategies, allowing the plant to live in very large soils conditions. This endemic tree species is currently threatened by the introduced psyllid, *Acizzia uncatoides*. The observed mortality recorded in the heights of the island, and observed lower impacts on the tree in the East are supported by our results. Knowing the ecology of the species may contribute to a better understanding of its resilience to the invader.

Keywords: leaf traits, ecophysiology, plants, elevational gradient, La Réunion

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Assessing the use of scientific floras as data sources for trait-based research in the Canary Islands

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The use of functional trait-based approaches in ecological research has gained momentum in recent years, enhancing our understanding of biodiversity and how it relates to ecosystem functioning. Such research often requires the collection of data on multiple traits from many species; obtaining these data requires time and resources, which are often lacking, particularly in conservation research. A wealth of information about species' characteristics can be found in the literature, including floras or other types of species identification books. This information can be especially valuable for geographic areas that are abundant in rare and endemic species, such as islands, for which detailed information is rarely known-such species tend to be missing from large online trait databases. Data from scientific floras are easily accessible and may act as valuable data sources to be used in conservation efforts. However, the data may have been collected by many different researchers using a range of methods and important functional traits (e.g. leaf area) are usually missing. The reliability, and thus usefulness, of such data therefore requires testing against trait values measured in the field using standardized methods. We use trait data digitized from the most recent and comprehensive guide of the Canarian flora, to determine how accurately they capture trait values measured in the field from the islands of Tenerife and La Palma. We test the accuracy of the trait data at estimating functional diversity of endemic and non-endemic species, while also comparing functional diversity between islands. We estimate leaf area using leaf length and leaf width, as obtained from the scientific flora, and compare this with precise measurements of leaf area from the field. Preliminary results suggest that leaf length and leaf width are sufficient for calculating leaf area. Overall, we find that data used in scientific floras underestimates functional diversity in the Canary Islands and that this is particularly true for rare endemic species. This may have important consequences for the conservation of unique species, which are often aided by the use of scientific floras.

Keywords: functional traits, Canary Islands, plants, guide books

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*Speaker

Variability of hydration traits in the *Ramalina decipiens* group (Ramalinaceae, lichenized Ascomycota): towards unraveling their adaptive role

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Adaptive radiations are paradigmatic examples of how biodiversity increases, and those occurring in oceanic islands are among the best documented examples. Plants, reptiles, birds and even spiders or insects are well studied in islands and archipelagos all over the world, but other putative cases of adaptive radiations may occur in other organisms. *Ramalina*, a genus of lichen-forming fungi with c. 200 species known worldwide, shows a high diversity in Macaronesian archipelagos (c. 40 species), coupled with high levels of endemicity (c. 50%). This figures are remarkable considering most lichen-forming fungi show very wide distribution ranges. Most of the endemic diversity belongs to two hypothesized radiations, which might have an adaptive basis. In this study, we focus on the *Ramalina decipiens* group, which shows its highest diversity in the Canarian archipelago and has several single-island endemisms in Porto Santo Island. The genus *Ramalina* is characterized by the ability to obtain water from fog and humid air. We hypothesize that one of the main drivers of the radiation in the *R. decipiens* group is that the species evolved differentiated ecophysiological strategies to exploit fog, based upon thallus anatomy and cell wall composition. In order to characterize these strategies, we studied hydration traits (specific thallus mass, water-holding capacity and water content), hydration and dehydration kinetics, surface hydrophobicity and thallus anatomy by means of light and scanning electron microscopy. Results are analyzed and discussed in a phylogenetic framework.

Keywords: Ecophysiology, hydration, lichen, forming fungi, Macaronesia, radiation

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Bird communities of the Mahavavy-Kinkony Wetland Complex, western Madagascar

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The wetlands and mangroves of the Mahavavy-Kinkony Complex protected area, northwestern Madagascar, host thousands of migratory birds each year and together with breeding populations of Malagasy birds, the community has exceptional species diversity. Although data are available on different monitoring sessions at the site, little is published on local bird diversity and ecological preferences. In the context of an ecological monitoring program, a study of bird community structure, and threats to species and habitats was carried out twice a year between 2015 and 2017 at four sites within the protected area to provide information for conservation and ecotourism programs. Based on general observations, censuses along rivers and the coast, and counting at fixed points, data on species richness, population size, and anthropogenic pressures were collected. A total of 69 species, including nine threatened species, were identified. Important aquatic, shorebird and marine populations were found, such as *Calidris ferruginea*, *Egretta ardesiaca*, *Plegadis falcinellus*, *Phoenicopterus minor*, and *Sterna bengalensis*. The Mahavavy River delta was found to have numerous species and large populations not found elsewhere in the protected area most likely associated with the vast intertidal area and mangroves. Several zones with high bird concentration were recorded, in particular the Ambavanatsatra intertidal zone, the Ambolodia swamp, the Antsoherimitabo islet, and Kinkony Lake. Although all the study sites are within the protected area, some anthropogenic pressures still persist, such as mangrove cutting for timber and firewood, and transformation of swampy habitats into agricultural and grazing areas. The enhancement of the site's exceptional bird diversity through an ecotourism program and the reinforcement of conservation actions are paramount to preserving the regional wetland ecosystems.

Keywords: bird communities, diversity, wetlands, mangroves, habitat preference

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Functional traits of vascular plants on islands across spatial scales

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Islands have served as prominent model systems in ecology and evolution in the last century and have sparked influential theories such as the equilibrium theory of island biogeography. A main limitation of neutral models like the equilibrium theory of island biogeography is that they consider islands as static entities and species as ecological equivalent. This view neglects two important notions of contemporary ecology and biogeography: i) that islands are highly dynamic systems and ii) that differences in species traits are key to advance our understanding of the assembly and evolution of species communities. As part of the DynaCom project, we aim at developing a quantitative functional island biogeography of plants by investigating the trait composition and functional diversity of island plants the global scale over the regional to the local scale. Specifically, we will investigate (1) the position of island plants in the global multi-dimensional trait space of plants using the GIFT database (gift.uni-goettingen.de), (2) how the trait composition and functional diversity of single islands and archipelagos is related to contemporary island characteristics and long-term dynamics (geological age, island ontogeny, LGM sea-level change), (3) how different facets of functional diversity can be predicted by equilibrium vs. non-equilibrium theories, (4) how colonization and speciation determine trait distributions and the structure of the trait space (functional richness, evenness and dispersion) of island assemblages, (5) how functional diversity and trait composition of small-scale plant communities are affected by broader scale processes operating at the whole-island and assemblage level.

Keywords: diversity, evolution, functional, plants, spatial, traits

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*Speaker

Conservation

Contents

Genomic structure of Black lemur populations and a long term conservation program at the Ampasindava Peninsula, north-western Madagascar

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Most threats on lemurs are connected to an increasing degree of habitat loss and fragmentation. Alarmingly, one in four lemur species is currently listed as either *Endangered* or *Critically Endangered* by the IUCN Red list. Madagascar is a large country and prioritizing conservation zones remains challenging both logistically and with regard to limited budgets. To approach this question, we have combined and applied methods from the fields of conservation genetics and conservation biology. Study was conducted in the Sambirano region, north-western Madagascar, where we identified *Eulemur macaco* populations from the remnant natural forest habitat. Three populations were subjected to whole genome study using next generation sequencing techniques with Illumina Hiseq platform. Sequences analyses were based in standard Illumina pipeline. After quality control and sequences cleaning pipeline, Sequencing reads were trimmed from the end of the read until the first base over Q10 and reads shorter than 40 bp were discarded. The Genome Multitool mapper was used to identify all alignments to available sequence reference in Genbank. Genetic diversity, homozygosity and genome characteristics have been evaluated to understand population structure. We have sampled four populations of *E. macaco* around the Sambirano region and we have been able to deep sequence six samples for the genomic study. Results show the importance of the population around Ampasindava peninsula with high conservation value. Therefore, this area has been set and prioritized as hotspot sites to develop a highly focused community-based conservation strategy for sustainable use of natural resources, starting from an environmental education program in public primary school. For the first phase, we have used locally-based information centers to train teachers how to use a particular scholar kit designed for Ampasindava called *Ma Jôby.* This tool aims at raising awareness of black lemur conservation and their natural habitat. Impact of the program was measured by analysing pupil's drawing before and after using the kit for few months. As preliminary results, less is known by the pupils about the value of the local biodiversity, in particular the uniqueness of Black lemurs, before the education program starting time.

Keywords: Eulemur macaco, conservation genetics, Ampasindava peninsula, environmental education, Madagascar

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Connectivity of island ecosystems from a management and ecological perspective

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Earth is home to over 100,000 islands, which support 20% of global biodiversity, but are also where 80% of known extinctions have occurred, making them some of the most important but vulnerable ecosystems in the world. Managing island ecosystems for biodiversity conservation has become increasingly challenging due to intense pressure from invasive alien species, habitat loss and, increasingly, from climate change. The role of connectivity to island ecosystems, or lack of, has played a major role in the evolution of these critical sites; connectivity enables gene flow between sites but increased connectivity has also led to increased anthropogenic threats. Island managers and conservation practitioners are tasked with understanding the role connectivity plays in the stability of their sites and use this understanding to improve management of threats and channel resources according to where they will be most effectively used. A greater understanding of the connectivity of island ecosystems, both from a management and an ecological perspective is therefore needed to maximise the effective management of island ecosystems. This is especially the case for Small Island Developing States (SIDS) where capacity and resource constraints (human, institutional, and financial) seriously impinge on national and regional responses to global environmental challenges such as global warming and biodiversity loss. This research aims to; i) determine the level of management connectivity/coordination among sites, the factors influencing effective management and how management could be improved; ii) determine the likely sources of coral population persistence within the Seychelles archipelago by developing a population connectivity map and (iii) quantify the threat of marine plastic pollution on Aldabra Atoll UNESCO World Heritage Site by investigating its accumulation rates, origins, and the proportion of debris with rafting biota. One outcome of this research will be to enhance the conservation management effectiveness of island ecosystems.

Keywords: Connectivity, Coral Reef, Seychelles, Effective management, Plastic Pollution

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*Speaker

Predictive habitat models integrating anthropic pressures to aid conservation of a rare species on Reunion island, the Mascarene petrel

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Conservation planning requires the identification of habitat that may support focal species, and an assessment of how to prioritise lands to protect sustainable populations. Because conservation plans often guide the allocation of limited resources in the face of habitat loss, there is little room for error in the prioritisation process. However, incomplete information on the distributions of species and habitats makes prioritisation an enormous challenge, particularly if surveys cannot be conducted due to land inaccessibility or other constraints. The use of predictive habitat distribution models by land managers in the conservation management of threatened species is therefore increasing. Reunion Island (western Indian Ocean) is one of the few islands at global scale holding two endemic species of petrels, the Barau's Petrel (*Pterodroma baraui*), and the Mascarene Petrel (*Pseudobulweria*), both of which are poorly known and endangered. The principal threats to both species are introduced mammalian predators (rats and feral cats) and light pollution. In this study, we focused on the very rare Mascarene petrel whose remained mysterious for 160 years. Thanks to the recent discovery of breeding sites in 2016, it is vital, to face conservation urgency, to quickly identify all potential breeding areas and engage actions at a broader scale. Thus, we used environmental parameters mixed with anthropic pressures (predators density and level of invasive plants) to investigate and model the distribution of suitable habitat of this rare and endemic species. Predictive distribution maps revealed habitat refuges suggesting a high sensitivity of the species to anthropogenic pressures. This approach is very helpful for long-term management to 1) identify priority conservation areas, 2) design concrete actions to be implemented according to the environmental / anthropic characteristics of the habitat.

Keywords: habitat modeling, endangered species, endemic species, conservation, tropical island

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*Speaker

Assessment of frugivorous bird populations in a naturally fragmented landscape by acoustic monitoring (Reunion, Mascarenes)

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Frugivorous birds play a crucial role in fleshy-fruited plant recolonisation of lava flows, but their population decline or fragmentation of their habitat may jeopardise the effectiveness of seed dispersal. In the naturally fragmented landscape of the Piton de la Fournaise lava flows, we ask: What is the diversity and the abundance of frugivorous bird species and is the spatial distribution of frugivorous birds related to the structure of the vegetation? We used two Song Meters (SM4) to monitor birds assemblages on Reunion at Le Tremblet. The SM4's were located on trees at 7 m height, on either side of the 1800 AD lava flow. Each SM4 has two stereo microphones that enable monitoring of acoustic activity on the 1800 AD lava flow where the canopy is low and open and on the older lava flow where the canopy is high and closed. Song templates were constructed for each species and automatic detection was performed. Preliminary results reveal that the most abundant frugivorous birds present at Le Tremblet are the exotic Red-whiskered Bulbul, Pycnonotus jocosus, and the Reunion Bulbul, Hypsipetes borbonicus. The Mascarene Grey White-eye, Zosterops borbonicus, which is a tiny opportunistic frugivore, the Malagasy Turtle-dove, Nesoenas picturata, which is mostly considered a seed predator and the exotic Common Myna, Acridotheres tristis, were detected to a lesser extent. Preliminary results also show that there is a lower number of detections on the 1800 lava flow where the canopy is open, especially for the Reunion bulbul. Frugivore birds at Le Tremblet show a low diversity and preliminary monitoring suggests that the most abundant species is the exotic Red-whiskered Bulbul, which mainly eats exotic fleshy-fruited species. The Reunion Bulbul is the biggest native extant frugivore on Reunion is also well represented, but this species might prefer old-growth forests and might therefore play a minor role as a seed disperser in open canopy areas.

Keywords: Bioacoustics, Biological invasions, Conservation, Ornithochory

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Monitoring terrestrial arthropod fauna for habitat knowledge and conservation in Réunion island

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Almost half of Reunion Island is protected by a national park and included on the UNESCO World Heritage List for its unique biodiversity. Arthropods, mainly insects, represent two thirds of biodiversity worldwide, and very likely on Reunion, and more than 75% of the animal diversity in non-marine ecosystems. Moreover, 31% of Reunion's arthropod species are endemic to the island and 40% of the Mascarenes archipelago. Data concerning arthropods collected using standardized protocols over 400 sites spread across the island for the last two decades were gathered to create spatialized, state-of-the-art knowledge on arthropod bidiversity. Standardized collections by vegetation beating and light trapping provide most of the information at both the island and at the major habitat scales, with valuable additional information on the relationship between arthropods and plants at species level. All the main habitats and altitudinal ranges were sampled but in a rather unbalanced way with a scarcity of information on the windward side of the island and associated habitats. In addition, when standardized, collections by vegetation beating allow us to quantify the relationship between arthropod biodiversity metrics such as richness, diversity or endemism, and plant species, habitats and their conservation level. These documented links are helpful tools to define conservation priorities, as well as to evaluate habitat disturbance or recovery. On permanent reference sites, such protocols, shared with other islands, can be implemented to define reference states for long term monitoring in the context of biological invasions and global climate change.

Keywords: arthropod sampling, traps, endemism, diversity, habitat level

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†Speaker

Knowledge and conservation of the unknown and threatened flora of Mayotte

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Since 1996, 43 new plant species have been described and are present in Mayotte (including 28 strictly endemic to Mayotte), a small island (374km^2) situated up North of the Mozambique Channel with a very high indigenous species diversity (1.8 sp/km^2). Numerous species present in MAO herbarium (*Index Herbariorum*) still have an undetermined status. A taxonomic work is thus necessary because those species are probably rare and endemic considering that only 5% of the local vegetation is still "primary" on the island (constant regression). The goal of this project was to identify undetermined taxa in MAO herbarium. To do so, we started an inventory and computerized all specimens (about 600 undetermined sheets). Among 30 presumed new species for science, we selected 12 species (*Diospyros sp. ; Gagnebina sp. ; Kedrostis sp. ; Colubrina sp. ; Camptolepis sp. ; Plagioscyphus sp. ; Dombeya sp. ; Habenaria sp. ; Erythroxylum sp. ; Kedrostis sp. ; Aloe sp. ; Volkameria sp.*) for which we collected new samples by fieldwork to determine chorology and phenology. For the first time in Mayotte, we start a silica gel and an alcohol collection to complement the herbarium and ex-situ collections. We solicited numerous experts worldwide (France, Belgium, UK, USA, South-Africa, Brasil, Sweden...): 25 answered favourably to help us with the identification. Some of the targeted species are already in the process of being published: *Diospyros pascalii* Lowry *sp. nov.*, which is endemic to Mayotte; *Gagnebina lewisii* Luckow *sp. nov.*, which is also present in the North of Madagascar, and *Dombeya rosaceae* Arène, which is known from only one locality in Madagascar and identified for the first time in Mayotte. This work highlights the need for taxonomic work in Mayotte as numerous species must still be described. A system has now been initiated on taxonomic work of the flora and this will allow us to integrate these species into conservation programs. This work was funded by BEST RUP program.

Keywords: Taxonomy, conservation, herbarium, Mayotte, new species

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*Speaker

Conservatoire Botanique National de Mascarin: an essential tool for knowledge, preserving and assisting decisions on the most endangered plants and habitats of La Réunion, Mayotte and IIes Eparses

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The Conservatoire Botanique National de Mascarin (CBN Mascarin) has existed for more than 30 years and is the only CBN in the French overseas territories. Its approved territory includes La Réunion, Mayotte and Iles Eparses, ranging from small atolls to high volcanic islands, located within the Madagascar and the Indian Ocean Islands global biodiversity hotspot area. For vascular plant taxa, 573 are threatened with extinction. The CBN Mascarin needs to preserve more threatened species in La Réunion than in metropolitan France, despite La Réunion being 200 times smaller. CBN Mascarin aims at coordinating major programs of knowledge on the flora and vegetation, preserving the plant heritage, supporting the State and local authorities in their planning policies, and finally working to raise awareness and educating all types of audiences on conservation issues. To prioritize and implement effective conservation actions on the threatened flora and habitats, it is compulsory to regularly update a lot of information, e.g. size of functional populations, adults/juveniles ratio, habitat conservation level. The work also focuses on technical means of growing native plants, in order to carry out *ex situ* collections and to achieve biological reinforcement of wild populations. The CBN Mascarin has developed a relational database, Flora indexes, Reference Herbaria, conservation plans, collaborative websites and an early detection and rapid response system to prevent new invasions. Around 30 expert botanists are also mobilized as partners. Communication and public awareness activities consist of the diffusion of videos and key information on social networks, travelling exhibitions and public reception. The *Mascarine Cadetiana* database currently contains 302 660 floristic observations and 300 natural habitat types. These data have been analysed in order to prioritize the threatened species and habitats across the three territories. More than 120,000 native plants have been introduced either in arboreta or *in situ* conditions. To date, only 18% of endangered species benefit from conservation measures, based on a conservation of flora and habitats strategy. To conclude, CBN Mascarin needs to keep on playing a major part *in the main issues of biodiversity knowledge and conservation in the* islands of the Western Indian Ocean.

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Keywords: plant conservation, knowledge, threatened native flora and habitats, La Réunion, Mayotte, Iles Éparses

Saving the Swamper: research and efforts for conservation of the endemic and critically endangered Utila Spiny-tailed iguana (Utila, Islas de la bahia, Honduras)

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The Utila Spiny-tailed Iguana (*Ctenosaura bakeri*) is endemic to the Honduran island of Utila, part of the Bay Island chain and the smallest of these islands at 41km2. Primarily a mangrove species, this Critically Endangered iguana inhabits the red, black and white mangrove swamps of the island, which cover around 8.74km2, and to a lesser extent, coastal hardwood forests. Due to this habitat preference, *C. bakeri* has earned the local name of 'Swamper' on the island. *C. bakeri* is protected under Honduran national law and, since 2010, listed on Appendix II of CITES. However, this law is rarely enforced. Furthermore, the consumption of iguana meat is considered traditional on the island and the mainland, with the poaching of gravid females containing eggs being a common threat. With an increasing human population on Utila, it is likely hunting pressure will also continue to rise in tandem. Consequently, this is a critical time for the conservation of *C. bakeri*, with environmental education and community engagement paramount to successfully preserving this species and its habitat.As the 'Swamper' is already known locally (albeit often as a delicacy), this presents an ideal opportunity to build on this knowledge in a more positive light and make the iguana a flagship species for wildlife conservation on Utila. Work in the last two years by Kanahau Utila research and conservation facility has sought to raise awareness about the plight of *C. bakeri* to tourists and residents alike. By highlighting the human impact on this species, we hope to create an umbrella effect that would help conserve island habitats and, consequently, many other species of conservation importance. To counteract the poaching of iguanas, and generally inspire an appreciation for local wildlife and ecosystems, it is essential that environmental education of the younger and current generation take place, and that it be effective, interactive and informative.

Keywords: herpetology, iguana, environmental education, conservation, community outreach

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[*] Speaker

Implementation of a sampling protocol for the delimitation of ZNIEF in Grande Comore island

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Comoros archipelago is among the 20 island states within biodiversity hot spots, in terms of global conservation priorities. Grande Comore is the largest and well-preserved island in the Comoros archipelago. Taking into account nature and the various natural and anthropogenic pressures, it is important to promote a management plan that would guide future conservation issues for the island's flora and habitats. Nevertheless, considering the fact that little data exists for the Comoros, it is necessary to develop a methodology that is both rapid and repeatable, in order to delimit the ZNIEFF (Natural Zones of Ecological, Faunistic and Floristic Interest) in Grande Comore Island. Given the urgent need to define a conservation plan in the Comoros, we have focused this study on the remnant forests of La Grille, on the northern side of Grande Comore Island, a choice motivated by the accessibility of this site and the size of its massif (300 km2). We have delineated the board units of vegetation by ortho-photography using QGIS software and existing data. This experimentation will be followed by a field survey using a ZNIEFF-type inventory, as well as a verification of the delimited areas based on the data recorded on the study site. It will then provide an approach on the state of conservation of remnant forests, the different types of pressures within natural and semi-natural habitats and the extent of existing threats, including invasion by exotic species. The approach defines areas of ecological interest and provides a management framework for prioritizing habitat conservation choices. It will thus serve as a decision-making support for future biodiversity conservation issues in the Comoros.

Keywords: hot spot, conservation priority, remnant forest, habitat, ZNIEFF

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Vegetation characterization, effect of prescribed fire and forage quality in insular savannas

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Réunions savannas have been under threat by exotic woody encroachment since the end of pastoral activities. A management plan combining prescribed fire and herbivory is under creation to preserve these areas and their uses. The objectives of this study are to: 1) Characterize the current vegetation and use this to 2) measure the impact of prescribed fires on the abundance of woody plants and the viability of seeds in the seedbank, and 3) determine the forage quality of 4 dominant species in order to introduce livestock and promote herbivory. Species composition, abundance and phenological state of woody species were recorded one month before the fire (October 2016) and 5 months after the fire (April 2017) in 10 permanents plots of 100 m^2. Seeds of fourty soil samples, taken before and after the fire, were allowed to germinate in phytotrons. Biomass was sampled in 28 plots of 0,25 m^2 for 2 dominant herbaceous species (*Heteropogon contortus* and *Panicum maximum*) and 2 dominant woody species (*Leucaena leucocephala* and *Vachellia farnesiana*) and their forage quality (NDF content, protein content) was measured by Near-InfaRed Spectroscopy (NIRS). Fifty-six exotics species and one indigenous grass species (*H. contortus*) were recorded. Twenty-seven % of the woody population died after the prescribed fire. Survivors show a great ability to resprout. Individuals of *L. leucocephala* with dbh ≤ 1 cm were more sensitive to fire than those with dbh > 1 cm and the abundance of its expressed seeds is greater after fire. The two Poaceae species have a higher NDF content and a lesser protein content than the two Fabaceae species. These grasses do not alone meet the nutritional requirements in energy and protein of dairy cows or goats. However, pasturing livestock in areas with an abundance of Poaceae and Fabaceae ensures the nutritional requirements of the animals are met (80 % Poaceae and 20 % of the Fabaceae species). Combining prescribed fires and herbivory by local breed livestock adapted to these natural environments may inhibit encroachment by exotic woody species by limiting seedling establishment and the regrowth of woody plants after fire.

Keywords: fire management, forage quality, germination, Leucaena leucocephala, savannas, shrub encroachment

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[*] Speaker

Biodiversity of terrestrial arthropods in Réunion island

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Together with Mauritius and Rodrigues islands, Reunion forms the Mascarene archipelago, which is included in the international biodiversity hotspot of Madagascar, a world leader in terms of both species endemism and habitat transformation. Because knowledge of Reunion's entomofauna was still incomplete or unpublished, an up-to-date census of Reunion's terrestrial arthropods was produced. Of the 3369 species that are reported for Reunion, 31% are endemic to Reunion and 40% are endemic to the Mascarenes. Moreover, a diversity ratio between the numbers of described and expected species in the world was established and then applied to the numbers of described species in Reunion to estimate the expected total numbers of species on the island. The results predict that between 6751 to 10812 species of terrestrial arthropods are present in Reunion and that 62% of species remain to be discovered. However, some groups appear underrepresented as expected for Darwinian islands that should originally be composed by species with abilities to colonize remote areas.

Keywords: arthropods, disharmony, endemism, regional pool, species richness

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†Speaker

Ecology on Islands

Contents

Mangrove ecology on an undisturbed atoll: diversity, structure and changes in extent over 30 years on Aldabra, Seychelles

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Islands and their endemic biodiversity are challenged by the progressive loss of suitable habitat as a result of sea level rise. In this research we assess changes in mangrove extent and species diversity on Aldabra Atoll-Seychelles' largest area of mangrove forest (1720 ha)-to understand the response of this protected habitat to a moderate but increasing sea level in the Indian Ocean. Plot-based diversity was surveyed in a large mangrove stand on the atoll with 39 plots of 25m2. On an atoll-wide scale, a post-classification change detection method (overlay of two independently classified images to derive extent change) was used on several Landsat surface reflectance images from 1985 to 2015. Three mangrove species were encountered in the survey; the most important (considering frequency, density and dominance) was *Rhizophora mucronata*, followed by *Ceriops taga*l and *Avicennia marina*. The tallest mangrove tree recorded was 8.10 m and the largest had a stem diameter of 47.4 cm (*A. marina*). The seedling density in the stand was 12,308 stems/ha indicating a high regeneration rate and recruitment. Results of the change detection reveal a net gain of 174 ha in mangrove area on Aldabra during the study period. The increasing trend was matched by dynamic mangrove vegetation, especially at their landward margins suggesting that mangroves on Aldabra are resilient, and persistent in colonising new suitable areas over time. Loss of established mangrove forests at their seaward margin was observed only on the northern, most exposed part of the coastal lagoon highlighting the importance of continued habitat monitoring. This work serves as a valuable baseline for understanding the ecology of mangroves on islands, and their response to climate change drivers in the absence of local human effects.

Keywords: mangrove, post classification change detection, Landsat, species composition, sea level rise

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Vertical distribution of birds in different dry forest types of western Madagascar

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The lowland forests of western Madagascar show notable variation in structure, which is correlated with local edaphic and bioclimatic conditions, and these aspects are accentuated along a north-south latitudinal gradient. Few data are available for Madagascar on the relationship between vegetation structure and bird assemblages, but this information is important to understand the evolution of these communities and associated habitat requirements. To fill the gap, aspects associated with the vertical structure of natural vegetation on bird richness, composition, diversity and abundance, particularly common species, was examined at three lowland protected areas along a latitudinal gradient: dry deciduous forest of Ankarafantsika (north-west) and Menabe Antimena (central-west), and spiny bush of Tsimanampesotse (south-west). Observations were made during the dry season from May 2017 to September 2017 using linear transects to survey birds and linear sampling to quantify vegetation structure. Ankarafantsika and Menabe Antimena showed similar patterns along different vertical strata, including species composition, and more specifically with the mid-story containing the highest bird species richness and abundance. In contrast, the habitat structure of Tsimanampesotse differs from the two dry forest sites, being more open and lower in stature, with the canopy has the highest species richness and the understory the highest abundance. Both dry forest and spiny bush habitats show similarities in bird species diversity index, which increases along a vertical gradient, with the upper strata have the highest values and an associated decrease in vegetation cover. The vertical distribution of the most common bird species differed significantly between the vegetation types. Vertical differences in the distribution of the bird communities can be explained by changes in vegetation structure, specific composition, bioclimatic conditions, resource availability, and different ecological factors. This study provides a foundation for future ecological studies on Malagasy birds.

Keywords: birds, strata occupation, deciduous dry forest, spiny bush, Madagascar

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Environmental heterogeneity as a driver of plant diversity on oceanic islands

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Oceanic islands are highly dynamic systems with complex geological histories and high environmental heterogeneity (EH). The General Dynamic Model (GDM) by Whittaker et al., (2008) emphasizes the linkage between geological dynamics and the rates of biogeographical processes on oceanic islands. In the GDM, EH, island area and species numbers are predicted to peak at intermediate island age. The GDM has received strong empirical support but one of its central propositions, that EH should follow a hump-shaped trajectory as the island ages, has never been empirically tested. In our study, we quantified EH on oceanic islands worldwide, tested the temporal EH trajectory and evaluated the importance of EH as a predictor for species richness and endemism of vascular plants on oceanic islands. We calculated 25 EH metrics capturing the different aspects of the heterogeneity of elevation, precipitation, temperature, heat load and terrain wetness for 136 oceanic islands belonging to 42 archipelagos. We summarized EH per island by its standard deviation, range and using neighborhood analysis (calculating standard deviation, roughness and dissection in a moving window). For testing the EH trajectory over time and its importance for species richness and endemism of vascular plants, we used linear mixed effect models. We found that several EH metrics were positively correlated among each other, e.g. heterogeneity of elevation and temperature, and metrics using range and standard deviation statistics. The EH peaked at an early stage of island ontogeny, rather than at intermediate island age as predicted by the GDM. We additionally found that certain metrics of EH exhibited a u-shaped trajectory over time. The EH improved the predictive power of GDM for both species richness and endemism. Models that included precipitation and temperature heterogeneity best explained species richness, while models that included elevation and temperature heterogeneity best explained endemics species. Our results provide empirical evidence for the GDM assumption that EH follows a hump-shaped trajectory over island ontogeny and show that including EH as a predictor variable into island species richness and endemism models improves model fits.

Keywords: oceanic islands, environmental heterogeneity, island ontogeny, species richness, endemism.

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Dioecy on the Canary Islands. Sex-ratio and sexual dimorphism in laurel forest trees

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Dioecy, or separate male and female individuals, is the most extreme sexual specialization in plants. Only _˜4-6% of flowering plant species are dioecious, however its incidence is much higher on island ecosystems (e.g. 21% of the New Caledonia's flora is dioecious). The origin of this sexual system on insular ecosystems can be an ancestral condition (the species was already dioecious when arrived) or a derived trait (dioecy evolved *in-situ*). Although dioecy has received considerable attention on many oceanic islands, it is surprising the lack of knowledge from Macaronesian archipelagos. A preliminary study suggests that a 75% of the dioecious species in Canary Islands might be originally dioecious. Specifically, the laurel forest at the Canary Islands stands out with a high level of paleoendemisms, and thus, it could also harbour the highest number of dioecious species. To assess differences in dioecy presence and its origin at the different island ecosystems, we reviewed sexual system of all the 705 native flowering plant species in the Canaries. In the whole archipelago, 12% of the genera had at least one species displaying some degree of sexual dimorphism (dioecy, gyno- and androdioecy, subdioecy, trioecy and polygamy). Most of the dioecious species had woody habit (93%), presence of inconspicuous flowers (70%) and fleshy fruits (60%). Finally, the laurel forest showed the highest incidence of dioecy (11.5% of its species presented sexual dimorphism). Additionally, we surveyed sex ratios of natural and reforested populations of *Morella faya* and *Ilex canariensis*, two dominant dioecious species in the laurel forest. Although there was a trend toward male-biased sex ratios in *Morella faya*, most of the populations did not show any significant departure from 1:1. However, *Ilex canariensis* showed a significant male-biased ratio in 2 of 4 populations. Besides, several populations of both species showed a significant departure from a random males and females distribution. These preliminary data provide the first steps to understand the reproductive ecology of key species of these degraded forests.

Keywords: dioecy, sex ratio, breeding system, reproduction ecology, canary Island, laurel forest, Morella faya, Ilex canariensis

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Changes in plant and soil microbial diversity along gradients of land management in São Miguel (Azores)

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The natural vegetation in many areas of the world has been replaced by pastures and monocultures, leading to profound changes in the soil and plant communities. Therefore, a more sustainable management is desirable for pastureland worldwide. The Azores are ideal to model those changes, with habitats ranging from semi-natural to completely artificial found at relatively small distances. Furthermore, more than 50% of the land use in the Azores corresponds to pastureland, with agroindustry being a relevant socio-economic sector. Additionally, 30% of land use is dedicated to the production of wood, with the monoculture of Cryptomeria japonica. This research study aims to test bioindicators capable of providing an integrated insight of the changes in soil microbial community in Azorean grasslands and forests. Samples were collected according a gradient of land management intensity (MI): High (corn rotation grassland and production forest), Medium (permanent grassland and exotic forest) and Low (semi-natural grassland and natural forest). Top soil sampling procedures followed standard protocols. Plant cover was estimated using three replicates of 2x2 m for grasslands and 5x5 m for forests. One to two leaves of all above ground plant taxa was collected as well as one representative specimen of each taxon. So far, two sampling seasons have been conducted, Winter 2018, Spring 2018, in a total of 72 samples. Winter 2019 sampling campaign is underway, with one more Spring sampling season to be performed, matching the periods of 2018, in a total of 32 samples. Preliminary numerical ecology analyses of grassland floristic data showed that, regarding plant cover, the sampled pastures can be assembled into four groups, indicating a clear gradient from low to high MI, but also the presence of rotation of monoculture in the high MI grasslands. Spring and Winter sampling don't appear to have significant difference on non-rotational fields, for the first year. This will allow the future study of the associated changes in microbial soil communities.

Keywords: Azores, pasture lands, plant communities, management intensity, ecology

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Correlates of the distribution of microendemic species in New Caledonia

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New Caledonia is considered as the oldest oceanic island (37Ma). As a biodiversity hotspot, it is characterized by extremely high richness of endemic species and extinction risk. In a previous study, we characterized the range and the frequency of micro-endemism in different taxonomic groups. We showed that 116 adequately sampled species endemic to New Caledonia have very narrow distribution ranges, and that this trend is pervasive to the majority of the faunal groups. Here we aimed at determining the environmental correlates of this distributional pattern. We considered 12 environmental variables plus the richness of non-microendemic species and two variables of sampling effort (number of collectors and road density). Land use and soil type were the most discriminant, highlighting their much higher frequency in forests on ultramafic soils. The most predictive variables were the richness of non-microendemic species and sampling effort, followed by precipitation of the wettest and the driest quarters and slope. It shows that the distribution of humidity along the year is a major determinant of diversification and speciation, and that the complex orography with steep slopes in many places and directions is a main source of environmental dissimilarity. It certainly plays a central role in the discontinuity of distribution ranges, isolating populations and leading to speciation. Sampling effort is higher in sites of easy access but with higher richness, so increasing the chances of finding microendemics, but the way richness influences sampling effort needs to be better studied. This study sheds light on the main environmental correlates of microendemism and offers a powerful tool for predicting and exploring microendemism in poorly known areas in urgent need of conservation decisions.

Keywords: New Caledonia, microendemic species, terrestrial fauna, sampling effort, Random Forest

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Ecological release and the impact of urbanization on bird communities in mainland and island avifaunas in the Caribbean basin

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Ecological release occurs when species expand their habitat use in low diversity regions, such has been demonstrated in comparisons of habitat occupancy by birds in islands in the Caribbean and comparable mainland areas. Because the avifaunas of Caribbean islands are dominated, relatively, by generalist species (ominivores vs. species which are principally granivores, frugivores, nectivores, insectivores, carnivores, etc.), we would expect less impact of urbanization on the composition of their avifaunas compared to mainland avifaunas. We reviewed the literature on mainland and island avifaunas in the Caribbean region and accessed data for five regions, two mainland regions from coastal Caribbean and three islands (Puerto Rico, Grenada, and Tobago) where species lists allowed us to distinguish between specialist and generalist species across a range of habitats. We then identified the most rural habitats (primary or secondary forest) and then compared the guilds found there to urban habitats ("residential" or "downtown gardens"). As expected from previous studies of ecological release in the Caribbean, similarity of avian communities in rural and urban areas was highest on islands and lowest on the mainland. Among avifaunas, ratios of generalist to specialist species (G/S) were $\leq$ 0.5 in mainland forests communities and nearly identical ratios were found in urban areas, indicating that generalists and specialist guilds were equally affected by urbanization. This result was surprising because we expected greater dominance of generalists in urban habitats, no matter the region. For island avifaunas, G/S was usually $>$ 1 (range = 0.72 – 2. 73), indicating a greater dominance of generalist species. Moreover, G/S were always higher in urban areas (1.25 – 2.73) in comparison to forest habitats nearby (0.72 – 1.48) indicating a greater relative occupancy of generalist species in urban areas on islands. Thus, effects of urban environments on consumer communities are clearly dependent on regional history and biogeography.

Keywords: bird communities, Caribbean, urban, specialization, habitat

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When it's hot and dry, fig wasps easily die

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Climate change, marked by increases in carbon dioxide and ambient temperature levels, have caused changes in plant-pollinator mutualisms. This is the case for fig trees and their specific pollinators, agaonid wasps. Fig trees are members of the Family Moraceae, which can only be pollinated by the fig wasps from Family Agaonidae. For this study, *Ficus nota* and *Ficus variegata* fruits, pollinated by *Ceratosolen notus* and *Ceratosolen* sp., respectively, were used. We aimed to determine whether temperature, humidity, and seasonality holds an effect on the longevity of both *C. notus* and *Ceratosolen* sp. Both species were collected during the dry and the wet season and were exposed to different temperature and humidity conditions in an incubator. The mean percent survival was measured and the lifespan of each wasp was taken into account. Results for both *C. notus* and *Ceratosolen* sp. for temperature and humidity were similar, showing that an increase in temperature and a decrease in humidity significantly decreased their lifespan. For seasonality, however, *C. notus* had a significantly lower lifespan in the dry season as compared to the wet season, while the lifespan of *Ceratosolen* sp. was not affected by the seasons. These results indicate that climate change can negatively affect the ecophysiology of different insect species, ultimately affecting plant-pollinator relationships.

Keywords: insect longevity, climate change, Southeast Asia, survival

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Comparative study of the floral resources used by the native honeybee *Apis mellifera unicolor* Latreille by melissopalynological approach in 2 natural forest ecosystems of the South-West Indian Ocean islands: Ranomafana (Madagascar) and Mare Longue (Réunion)

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The natural forest ecosystems of the Southwest Indian Ocean (SWIO) have been strongly impacted by deforestation and face many biological invasions that can alter their balance, particularly plant-pollinator interactions. It is in this context that this study, describing the relations between an indigenous general pollinator: *Apis mellifera unicolor* and the flora of two ecosystems of Madagascar (Ranomafana) and Reunion (Mare Longue). To answer it, the inventories of the floral resources collected by the honeybee (nectar and pollen) and the survey of the available floral resourceswere carried out monthly. At Mare Longue, 120 species (53% exotic)were followed. In the honey samples, 53 species were identified, and 46 species in the pollen pellets samples. 24 species were common between honeys and pollen pellets. 35% of the species followed in the transects were found in the samples (honey and pellets). In quantity, the indigenous species, belonging especially to the tree or shrub's layer, were more visited than the exotic species. At Ranomafana, 131 species (95% indigenous) were surveyed. In the honey samples, 77 indigenous species, especially of the trees or shrubs, were identified. The indigenous species account for 79% of the species identified in the honey samples. 38% of the species followed in the transects are found in honey samples. For the pollen pellets, 13 634 pellets were analysed.100% of the samples were monospecific and was represented by 37 species (97% indigenous and 53 % belonging to the tree, shrub and liana layer). All these results confirmed the general behaviour of *A. m. unicolor*, with, however, a strong and significant preference for native floral species of tree and shrub layer and makes it possible to speculate on the important place of this bee in the ecosystems of the SWIO biodiversity hotspot.

Keywords: *Apis mellifera unicolor*, foraging behaviour, honey, native flora, pollen

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Ontogenetic variation in the effectiveness of *Gallotia galloti* as a seed disperser: implications for the conservation of the thermo-sclerophyllous shrubland of Tenerife

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Lizards in island environments tend to feed mainly on plants, therefore, they are considered as key elements for plant dynamics in many islands. In the Canary Islands, it has been shown that *Gallotia* lizards are among the most important seed dispersers of fleshy-fruited plant species. However, we do not know if lizards' effectiveness as seed dispersers change significantly throughout their ontogeny. Hence, we compared the seed dispersal effectiveness (SDE) provided by adult and juvenile individuals of *Gallotia galloti* lizards to a group of plant species representative of the thermo-sclerophyllous shrubland, one of the most threatened habitats in the Macaronesia. The objectives are *(i)* to assess if adult lizards disperse a higher number of plant species than juveniles, *(ii)* to compare the quantity and quality components of the SDE provided by adult and juvenile lizards. We characterized the seed rain mediated by adult and juvenile lizards in a population located in Tenerife (Canary Islands). We identified and counted seeds contained in lizards' droppings to assess the quantitative component of seed dispersal. To assess the qualitative component of dispersal, we considered the direct effect of lizard gut treatment on seed germination and the indirect effect of microhabitat suitability for seedling recruitment. The SDE was calculated as the product of the quantity and quality components of dispersal. Adult lizards dispersed a higher number of plant species than juveniles. Quantity of dispersal was higher for adult than for juvenile, whereas differences in the quality varied among plant species. Adults dispersed seeds mostly to exposed microhabitats, whereas juveniles mostly dispersed seeds under canopies. Our findings entail implications in the subsequent probability of seed germination seeds and seedling survival. Adult and juvenile lizards showed well-differentiated roles in the dynamics of natural regeneration of the thermo-sclerophyllous shrubland. If we consider that this difference is mainly due to body size, our findings would have important implications for the conservation and demographic dynamics of the thermo-sclerophyllous shrublands of Tenerife in the current scenario of global change, in which introduced predators are causing reductions in the body size of Canarian lizards.

Keywords: lizards, oceanic islands, ontogenic variation, plant conservation, seed dispersal

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Evolution on Islands

Contents

Independent phylogenetic origins of populations of the frog *Mantidactylus ambreensis* in the Montagne d'Ambre massif, northern Madagascar

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Madagascar is home to a considerable number of micro-endemic taxa and the manner local faunas have been assembled through the processes of colonization and species formation have rarely been studied. Here we analyse the phylogenetic relationships of the frog *Mantidactylus* (*Ochthomantis*) *ambreensis* (family Mantellidae), originally described from Montagne d'Ambre National Park (MDA) but also known from other sites in northern Madagascar. We used a large dataset of partial sequences of the mitochondrial 16S rRNA gene to assess the main lineages of *M. ambreensis* and related species in the subgenus *Ochthomantis*, and then used concatenated DNA sequences of four mitochondrial genes to infer the phylogenetic relationships among representative individuals of these lineages. Our analysis confirms *M. ambreensis* as monophyletic and composed of two main deep lineages, separated by 5.6-6.8% 16S uncorrected pairwise distance, and co-occurring on MDA. One of the main lineages is restricted to high elevations (941-1375 m a.s.l) on MDA, while the second lineage occurs at lower elevations (681-965 m a.s.l) on the massif, as well as in other humid forests of the north, but with deep divergences (up to 1.5% in 16S) among populations. Complete lack of haplotype sharing in the nuclear Rag-1 gene between these lineages at MDA despite micro-sympatry provides compelling evidence that they are separate species, though extensive morphological and/or molecular analyses of the type specimen are needed to taxonomically revise this complex and assign the name *ambreensis* to one of the lineages. Within the Low Elevation lineage, the MDA population is deeply nested among three other phylogroups with southern populations being more basal to those in the north. We therefore hypothesize that the MDA High Elevation lineage represents a relict population formerly widely distributed across northern Madagascar before being restricted to high elevations on this massif through vicariant speciation, followed by a secondary colonization of MDA by the Low Elevation lineage. The frequent parallel discoveries among frogs of closely related species with overlapping distributions brings to the forefront the manner species formation and ecological speciation took place, perhaps through specialization, across the high mountains of Madagascar.

Keywords: *Mantidactylus ambreensis*, Montagne d'Ambre, Ochthomantis, phylogeny, syntopic cryptic species

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*Speaker

Endangered marriage: Ecological genomics predict climate vulnerability in a lichen symbiosis

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Local adaptation is a critical evolutionary process that allows organims to thrive in their local habitat and results in species-wide geographic patterns of adaptive genetic variation. For symbiotic species such as tripartite lichens formed by a fungus, a green alga and a cyanobacterium, the spatial genetic heterogeneity of each of the partners can shape the ability of the lichen to respond to rapid climate change. Tripartite lichens play a key role in the Arctic and sub-Arctic where dinitrogen fixation by the cyanobacteria can contribute up to 80% of the nitrogen input into these nutrient-limited ecosystems. Climate change is more pronounced at these high latitudes than in other parts of the planet, being more than double in rate and magnitude in the Arctic than the global average. Here, we use ecological genomics to assess the potential for adaptation to rising global temperatures and precipitation for each of three symbiotic partners forming the widespread lichen *Peltigera leucophlebia* in Iceland. Using genotyping by sequencing, we identified single nucleotide polymorphisms in the three partners from 135 individuals across 27 sites in Iceland. We found that spatial patterns of genetic variation were most strongly associated with precipitation in the wettest and driest quarter and with mean annual temperature, and that the importance of these climatic factors for the observed genetic variation differs between symbiotic partners. Then, we estimated vulnerability based on genotypes i.e. the mismatch between current and predicted future genotype-environment relationships, using Gradient Forests, a nonlinear multivariate model. Our results predict areas most sensitive to climate change in Iceland, where *P. leucophlebia* populations will have to adapt the most to keep pace with regional climate change. After controlling for historical genetic structure, we detected links between climate-associated genotypes and genes important for enviromental tolerance in these organims, identifying potential mechanisms for adaptation to climatic changes in each of the lichen partners. By incorporating genotype–environment relationships into landscape-scale models of climate vulnerability, we predict that the three partners will respond differently to climate change. Our results should thus help to understand the evolution and fate of this ecologically important symbiosis.

Keywords: climate change, adaptation, symbiosis, lichens, ecological genomics, arctic and subarctic

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Genetic diversity associated with anagenesis and cladogenesis in Robinson Crusoe island (Juan Fernández Archipelago, Chile) and its use in conservation strategies

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The Juan Fernández Archipelago, located at 667 kms west of continental Chile, consists of three islands, Robinson Crusoe, Alejandro Selkirk, and Santa Clara. Its high level of endemism has allowed its designation as a World Biosphere Reserve and biodiversity hotspot. The development of this unique flora has been influenced by in-situ speciation processes, particularly anagenesis (phyletic speciation) and cladogenesis (associated with adaptive radiation). These processes have impacted levels of genetic diversity within endemic species of the archipelago, leaving different genetic signals within and among populations. This genetic diversity may have been affected by natural and anthropomorphic causes. In particular, the introduction of exotic plant species has pressured the native flora and resulted in an increase in the number of endemic plant species belonging to the Critically Endangered category (IUCN). This study evaluates the genetic diversity of species that have originated via cladogenesis (*Gunnera peltata* and *G. bracteata*, Gunneraceae), and anagenesis (*Dysopsis hirsuta*, Euphorbiaceae; and *Ugni selkirkii*, Myrtaceae) in comparison with parental species on the continent: *G. tinctoria*, *D. glechomoides* and *U. candollei.* The objectives are to examine differences in genetic signatures (from MIG-seq and AFLP) resulting from both processes, and also to use the genetic data to help suggest areas of interest for conservation. The results from a sample of 35 populations and 460 individuals show lower genetic diversity in relation to continental close relatives in the cladogenetically derived species, *G. peltata* and *G. bracteata*, but very similar values in the anagenetically derived species, *D. hirsuta* and *U. selkirkii.* Neighbor-net analysis indicates a clear separation between and among congeneric species, but not among populations of each of them on Robinson Crusoe Island; Structure analysis assigns three genetic groups for *Gunnera* and two groups for *Dysopsis* and *Ugni.* Based on this data set, the places on Robinson Crusoe Island that are considered priorities for conservation of these species are Quebrada Villagra, Plazoleta El Yunque, and sector La Piña. The authors thank FONDECYT Project 1160794 and CONAF Juan Fernández Archipelago National Park.

Keywords: genetic diversity, speciation, SNPs, AFLP, conservation

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The lichen flora of the MIOI (Madagascar and Indian Ocean Islands): results and perspectives

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The lichen flora of tropical areas is still poorly known, and entire regions, especially in Africa, lack even basic checklists. We conducted several field trips in the Mascarene archipelago, concentrating our efforts on Madagascar and Reunion. We started detailed taxonomical, phylogenetic, and biogeographical studies of lichenized fungi, based on a combination of morphological and DNA-based molecular data, and state-of-the-art methods and models. We further analysed the interactions between partners of the lichen symbiosis (fungi, green algae and cyanobacteria). The main outputs of this project are: *(i)* a preliminary checklist of lichens in Reunion now available, *(ii)* new species found in all groups examined; best examples are in the genus *Micarea* (13 species described as new for science out of a total of 21 species detected) and in the genus *Parmotrema* and a new genus (*Savoronala*) described from Madagascar, *(iii)* Interesting biogeographical connections: several species endemic to the southern hemisphere found (examples: *Gomphillus morchelloides, G. pedersenii, Sporopodiopsis mortimeriana*);strong connections with East Asia (examples: three new species of *Sticta* first discovered in Reunion, were eventually collected in Taiwan; *Micarea cilaoensis* first described from Reunion is common in Japan and Taiwan). A large and impressive radiation is zevidenced in the genus *Sticta* in Madagascar and the Mascarene arose from diversification following a single colonization event (c. 11 Mya), comprising 31 species, all but three have a very limited range, being endemic either to the Mascarene or a single mountain massif in Madagascar ; work with B. Goffinet. All but 5 are new to science. Laso, several fascinating interaction patterns between the partners of the symbiosis have been first demonstrated on specimens of Pannariaceae from Reunion: several bipartite lineages (fungi with cyanobacteria) derived from tripartite ancestors (including fungi, a green algae and cyanobacteria) and drastic changes of thallus morphology resulting from switches between different cyanobacterial symbionts. The lichen flora in Madagascar lives up to expectations regarding the island's biodiversity and endemism. The impressive diversity discovered on the young and tiny island of Reunion suggests that its great diversity of ecological niches allows for very high colonization rates from nearby islands and continents.

Keywords: lichenized fungi, taxonomy, phylogeny, biogeography

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Evolution of dioecism in Hawaiian Psychotria species

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Evolution of dioecism from hermaphroditism is frequently reported for plant species from oceanic islands, which implies an advantage for breeding systems that promote outcrossing on islands. Hawaiian *Psychotria* (Rubiaceae) consist of eleven endemic species, all thought to be derived from a single colonization event. The ancestor was thought to be distylous, and the extant species dioecious, though their functional breeding systems and the evolutionary pathway had remained unclear. This case is especially interesting because selective pressures for this proposed evolutionary transition are in question, since both distyly and dioecy require outcrossing. Aims of this study are to understand the breeding systems and pollination of Hawaiian *Psychotria* and to reconstruct their evolutionary pathway using molecular phylogenetic data. We examined floral traits of eleven Hawaiian *Psychotria* species and observed flower visitors in the field. Then we estimated the trait evolution combining the data obtained in this study and published molecular phylogenetic data. Although all three species in older sect. *Pelagomapouria* had flowers with longer styles exserted from corolla tubes and shorter anthers, two (*P. grandiflora* and *P. hobdyi*) were functionally gynodioecious while the other (*P. hexandra*) was subdioecious (leaky dioecious). The two gynodioecious species seem to have adapted to birds (likely Hawaiian honeycreepers) based on their floral morphology and nectar volume/composition, whereas *P. hexandra* appears adapted to moths. Meanwhile, all eight species in younger sect. *Straussia* were functionally subdioecious and appear adapted to insects with relatively shorter mouthparts. Considering their phylogenetic background, morphological traits, and the breeding systems, we hypothesize that the original colonist experienced the breakdown of distyly into monomorphy before colonizing the Hawaiian Islands, then evolved subdioecism through gynodioecism in the Hawaiian Islands. Furthermore, based on molecular dating and the current species distributions, both adaptation to the Hawaiian honeycreepers (*P. grandiflora and P. hobdyi*) and evolution of tiny flowers (sect. *Straussia*) have probably occurred almost sympatrically on Kauai Island.

Keywords: dioecy, heterostyly, Hawaii, pollination, plant breeding system

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Diversity of aphyllous Vanilla species in the south-west Indian Ocean region: a challenge for orchid taxonomy, evolution and conservation research

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The pantropical genus *Vanilla* is a member of the Orchidaceae family, one of the largest and most ancient families of angiosperms in the world. It originated in America and differentiated in America, Africa and Asia. About 126 species of *Vanilla* have been catalogued since the discovery of the genus*:* 25 can be found in Africa, 31 are indigenous to Asia, New Guinea and Pacific islands, and 70 are distributed in tropical America. The south-west Indian Ocean (SWIO) region, a biodiversity hotspot for orchids, is home to 9 native species of the genus with 7 aphyllous species and 2 leafy species. These 7 aphyllous are represented by two species with yellow flowers (*V. humblotii, V. perrieri*) and five species with white flowers (*V. madagascariensis, V. bosseri, V. decaryana, V. phalaenopsis, V. roscheri*). Recent molecular phylogenetic studies showed that these aphyllous species form a recent monophyletic group. Morphological descriptions of these aphyllous species in databases (MNHN, RBG Kew, Tropicos..) and in scientific publications are based on a limited number of individuals. The morphological traits (petals, sepals, label, and stems) are very similar between species and do not provide reliable identification despite possible flower size differences. Moreover, the species have more or less the same flowering period (October-December) and their geographical distribution areas overlap in Madagascar, increasing the probability of finding some sympatric species such as *V. madagascariensis, V. bosseri and V. perrieri*, and therefore possible hybrids. As the available information on genetic structuring and phylogeny of these species is insufficient, the resolution of their taxonomy is problematic. Aphyllous *Vanilla* species from the SWIO islands are thus an excellent model for understanding the evolution of orchids. For their conservation and to confirm the identity of these aphyllous species, an integrated approach with classical taxonomy using a large number of samples, intense fieldwork on biology and ecology, and molecular studies using variable markers is currently underway.

Keywords: Vanilla, Orchidaceae, morphological diversity, taxonomy, south west Indian Ocean region

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Evolution of pesticide resistance in invasive versus indigenous agricultural pests in an insular tropical environment

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Insular environments are among the most vulnerable ecosystems in the world, partly due to their small size and isolation. In La Réunion, an island in the southwest Indian Ocean, three whitefly species of the *Bemisia tabaci* (Gennadius) complex of cryptic species coexist: the indigenous species IO, and two exotic invasive species MEAM1 and Med, introduced in the late 1990s and in the early 2010s, respectively. *B. tabaci* is a major pest distributed worldwide, and a vector of plant viruses, responsible of serious damages on crops. The generalization of the use of pesticides has led to the emergence and rapid evolution of resistance in whitefly populations. In other countries, MEAM1 and Med have already demonstrated high resistance levels to all of the important classes of pesticides. Our objectives were to understand indigenous versus invasive whitefly species distribution in La Réunion, according to the different ecosystems; and how it could be linked to selection pressure of pesticide treatments. To assess species distribution, whiteflies were sampled at 59 collection sites, located all over the island in agroecosystems and natural areas. Molecular (kdr mutation, conferring Pyrethroid resistance) and laboratory bioassays (on three main classes of pesticides: Neonicotinoids, Pyridine azomethine derivatives and Pyrethroids) approaches were conducted on part of the sampled populations to assess pesticide resistance. The indigenous species IO was mainly sampled in natural areas and was found to be sensitive to the three classes of pesticides tested; in addition, no kdr mutation conferring Pyrethroid resistance was detected. The two exotic invasive species MEAM1 and Med were dominant in agrosystems. Most of the MEAM1 populations were found to be resistant to the three classes of pesticides tested, and kdr mutation was detected in both invasive species. Our results are in line with resistance cases reported worldwide in the literature, and suggest that whitefly species distribution in La Réunion could be driven by selection pressure of pesticide treatments.

Keywords: Bemisia tabaci, insular environment, biological invasion, species distribution, pesticide resistance

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Genetic traits affect the occurence and speed of island radiations - insights from an individual-based model

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Species radiations on islands have fascinated biogeographers throughout history. It is still unclear why particular lineages diversify, while others remain monospecific. The increasing availability of genetic data presents a new opportunity to shed light on this matter. This is particularly true in combination with ecological traits (e.g. body mass, dispersal abilities), which can reveal interactions between genetic and functional divergences. However, large scale sampling of fine scale genetic and functional data is next to prohibitive across islands and taxa for any useful generalization. Here we overcome this limitation by applying a genomically-explicit individual-based model for insular floras to assess the interaction between genetic and functional traits on lineage differentiation. In our model individuals of randomly generated species from the mainland can disperse to the initially empty island and subsequently adapt, differentiate and diversify. We analyse diversification patterns of lineages taking into account several genetic and genetically-coded ecological traits. While lineages with a low degree of genetic linkage manage to differentiate quickly into very specialized subpopulations, lineages with a high degree of genetic linkage remain initially species poor. After a certain period of accumulating mutations, however, those latter lineages go through a radiation burst, eventually surpassing species numbers of low-linkage-lineages. These findings suggest a two-phase-pattern for island diversification: an initial phase dominated by differentiation of lineages with low linkage level and a late phase dominated by differentiation of lineages with high degree of linkage. Our results provide insights as to what combinations of genetic and ecological traits distinguish species poor from species rich lineages. The identified trait syndromes combine three biological fields (genetics, ecology and evolution) to generate a series of hypotheses for empirical studies: from checking real-world trait syndrome (for model validation) to forecasting future diversification potential in a species impoverished but neobiota-rich world.

Keywords: island radiation, speciation, genetic hitchhiking, individual, based model, differentiation

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Crossing the speciation threshold: evolution in a complex archipelago

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Ever since Darwin and Wallace, island populations have been pivotal in understanding how new species evolve. The birds of Sulawesi, Indonesia, represent an ideal study system to examine evolutionary processes across islands and species. A region of complex biogeography and high endemism, the systematics of Sulawesi's fauna remains poorly understood. We have been looking at genetic patterns in bird populations across southeast Sulawesi, using barcoding genes ND2 and ND3. Different species show different patterns of isolation, as certain species can more easily cross between islands. The genetic work is supported by analyses of morphology and song. The patterns of isolation suggest that wingspan is not the only important aspect of bird biology which determines movement. Awareness of the drivers of isolation may help predict which populations are most likely to undergo allopatric speciation. We hope our discoveries will inform conservation efforts of the unique ecosystems they reveal.

Keywords: Sulawesi, Indonesia, birds, avifauna, dispersal, isolation

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Species delimitation and morphological evolution in two New Caledonian endemic genera of Papilionoideae (Fabaceae)

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New Caledonia (NC) biodiversity is rich and unique (75% of the vascular flora is endemic). Terrestrial plant diversity has been thoroughly investigated in this island leading to a better knowledge of the crucial influence of the environment (e.g. climate, soil) on plant communities. The legume family (Fabaceae) is represented in NC by c. 100 species. The most speciose clade of Papilionoideae distributed on this island is less than 10 Ma old and consists of two endemic genera, namely *Arthroclianthus* Baill. (13 spp.) and *Nephrodesmus* Schindl. (4 spp.). The distinction among these 17 morphologically-defined species remains challenging. Additionally, a recent study showed that none of these genera was monophyletic, but that they both belonged to the same clade. Observations conducted in the field lead us hypothesize that hybridization events could have occurred during the evolution of the group. Our objective is to clarify the systematics of the clade *Arthroclianthus-Nephrodesmus* within the subfamily Papilionoideae. We will present preliminary phylogenetic results based on the analysis of one nuclear and one plastid marker on an exhaustive species sampling. Ecological preferences and fruit and flower morphological-anatomical evolution in the clade will then be re-interpreted and help formulating new species delimitation hypotheses. This work will eventually provide the necessary data to 1) conduct a thorough taxonomic revision of the clade, 2) better understand the relationships of these endemic species with their pollinators, and 3) propose accurate conservation policies.

Keywords: endemism, legumes, systematics, flower and fruit morphology, New Caledonia

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Intra-island assembly of soil biodiversity: habitat filtering and micro-endemicity across space and habitats

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The spatial scale of speciation depends on the dispersal capabilities of organisms. In this sense, oceanic islands offer an interesting arena where taxa need to arrive over long distances and then colonize and adapt through the limited available space. The soil is inhabited by a small fauna of arthropods, most of them with strong dispersal limitations i.e. apterous species adapted to special soil conditions, which in the continent results in pronounced microgeographical structure of endogean diversity. Here we use community DNA metabarcoding to study mesofauna of Acari, Collembola and Coleoptera in samples from the four main habitats across the island of Tenerife (Canary Islands). Our results point to a massive diversity of soil mesofauna within the island, with communities associated to habitat type and with many soil lineages showing a strong geographic structure and microendemicity. These results shed light on the magnitude of long distance dispersal by soil mesofauna and while highlight the existence of extremely high levels of soil biodiversity and endemicity on oceanic islands potentially linked to important intraisland dispersal limitations.

Keywords: metabarcoding, soil biodiversity, scale of speciation

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Morphologically ”diskinkt”: comparing island populations of skinks in the Comoros archipelago

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Studying island radiations of species helps us better understand the ecological and evolutionary forces behind diversification following island colonization. This study focuses on a radiation of fossorial skinks of the genus *Flexiseps*, which is endemic to Madagascar and the nearby Comoros Archipelago. Specifically, I highlight *Flexiseps ardouini,* native to northern Madagascar and *F. johannae,* the only extant non-Malagasy species of *Flexiseps*, which is endemic to the Comoros Archipelago. A previous DNA barcoding study on Comoran squamate reptiles based on mitochondrial genetic data found *F. ardouini* nested within *F. johannae*, which was unexpected due to the allopatric distribution ranges and clear morphological distinction of the two species. The goal of my study was to investigate whether further morphological and nuclear genetic data confirmed this relationship. I found significant morphological differences among the four island populations of *F. johannae* and between the two species in morphometrics, pholidosis, and osteology, thus confirming the morphological distinction between *F. johannae* and *F. ardouini.* Some of the morphological differences between the species were size-related; I found *F. johannae* to present similar morphometric characteristics to *F. ardouini* just on a smaller scale, suggesting insular dwarfism in the Comoran species. On the other hand, the two species shared identical haplotypes in both nuclear genetic markers studied. This incongruence between genetic data and morphology perhaps indicates either a historical human introduction or a recent natural dispersal of *F. johannae* from Madagascar followed by rapid morphological adaptation to the environments of the Comoros. The morphological variability of *F. johannae* is unique for skinks and could be evidence of incipient speciation. *Flexiseps johannae* in the Comoros Archipelago is, therefore, an excellent new system for the study of island biogeography of terrestrial reptiles.

Keywords: morphology, herpetology, Scincidae, Madagascar, Comoros islands

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[*] Speaker

Towards a methodological unification and theoretical synthesis in Island Biodiversity Genomics: the iBioGen consortium

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Biodiversity genomics is a new and fast-growing discipline that uses large-scale DNA data to study species diversity and the processes that generate and maintain this diversity. Genomic technologies have enormous potential for establishing efficient biodiversity monitoring of island communities, in an effort to mitigate the impacts of global change and the spread of invasive species. Furthermore, the analysis of island communities under the framework of biodiversity genomics allows to integrate insights from ecological and evolutionary theory, towards a better understanding of island biodiversity dynamics across space and time. However, such a synthesis of biodiversity genomics is currently delayed by insufficient coordination among empirical biologists, bioinformaticians, and theoreticians and by lack of standardization of methodologies, which complicates comparisons among genomic datasets from different island systems. Here, we present iBioGen ("Twinning for European Excellence in Island Biodiversity Genomics"; *www.ibiogen.eu*), an EU-funded consortium bringing together experts in genomic technologies, island biodiversity and theoretical modelling research in order to (i) promote protocol unification and efficient integration of ecological field survey methodologies and genomic pipelines, (ii) establish a network of Genomic Observatories for long-term monitoring of European island biodiversity, and (iii) enhance a methodological and theoretical synthesis of biodiversity genomics, with a special focus on island biodiversity theory. Although the core team of iBioGen has broad expertise in island arthropods, we aim to further expand our approach to the full spectrum of biological diversity, by engaging with researchers working on a wider range of taxonomic groups from terrestrial, freshwater and marine island ecosystems. Thus, this communication will facilitate interactions of iBioGen with the broader island biology community, potentially forging new collaborations. We are also interested in interactions with island conservation scientists and practitioners towards an efficient integration of new technologies in biodiversity monitoring and conservation practices. This poster will present the main objectives and ongoing activities of iBioGen and will detail the forthcoming networking and training events organised by the consortium, including international symposia, working groups, and summer schools, which could be of interest to island biologists of different career stages.

Keywords: genomic observatories, high throughput sequencing technologies, island biodiversity, long term biodiversity monitoring

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Unraveling the role of habitat persistence in shaping population structure and demographic history across an island archipelago

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It has been suggested that habitat ephemerality selects for higher dispersal propensity, resulting in weaker population structure, in contrast to long-term habitat stability, which promotes lower dispersal and therefore higher population differentiation. Alternatively, habitat instability may cause repeated population bottlenecks leading to strong population differentiation due to genetic drift. Support for either of these hypotheses remains limited due to scarcity of suitable study systems, primarily because most species differ in a variety of traits apart from habitat preference. Here we focus on two insular lineages of the Eastern Mediterranean beetle genus *Eutagenia* (Coleoptera: Tenebrionidae), which occupy uniform climatic and trophic niches and have equivalent inherent dispersal capabilities but they differ in soil-type preference: the sand-obligate lineage is associated with unstable sandy coastal habitats, while the compact-soil lineage is associated with comparatively stable inner habitats. We sampled 'sand' and 'soil' populations of Eutagenia from eleven central Aegean islands and performed side-by-side comparisons of genetic diversity and population structure using genome-wide SNP data ($\approx$8000 loci, generated by ddRADSeq). Furthermore, we applied coalescent analyses based on the Site Frequency Spectrum (SFS) to compare demographic parameters and evaluate the relative contribution of bottlenecks and gene flow in shaping the observed patterns of genetic variation. Our analyses identified strong population structure for both lineages, but consistently higher population genetic diversity and deeper interpopulation divergences in the soil lineage. Moreover, population structure of the soil lineage corresponded substantially with Aegean paleogeography, in contrast to the structure of the sand lineage. The coalescent approach revealed a consistent and contrasting pattern between the two lineages: continuous population growth for soil populations, versus bottlenecks for their sand counterparts; coinciding with Quaternary sea-level changes. Even though both sand-obligate and compact-soil lineages present structured populations, distinct habitat-induced processes shaped their genetic structure. The apparent structure of sand populations is shaped by extinction-recolonization events, while the structure of the soil populations can be attributed to isolation due to island separations. Overall, our study suggests that habitat persistence indeed affects population dynamics, while exemplifying the potential of comparative population genomics for elucidating the role of ecological traits in the evolution of insular lineages.

Keywords: dispersal, demographic inference, habitat stability, Aegean islands, population genomics, Tenebrionidae

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A new multilocus phylogeny of the endemic Scincinae lizards of Madagascar reveals their biogeographic history and provides insight into their fossorial evolution

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Madagascar is one of the richest biodiversity hotspots with a significant proportion of its flora and fauna being endemic to the island. Skinks of the subfamily Scincinae form one of the most species-rich clades of squamates on the island. This group comprises 63 currently described species and several candidate new species. Within Madagascar they succesfully colonized most of the terrestrial ecosystem and they are characterized by a large morphological variability, underlying their multiple eco-morphological adaptations. Besides some species are known to be widespread and locally abundant, a significant proportion of the species belonging to this radiation are known only from one or a few individuals and localities. Profiting from a comprehensive molecular dataset comprising 13 loci and 80% of the described species (plus all known candidate new species, 12 of which are analysed for the first time), we compiled the most complete species-level phylogeny, and compiled a revised distributon dataset to study the historical biogeography of this clade. We then compiled a trait matrix that categorized the development of the fore- and hind-limbs of each species and their life-style (Fossorial vs Non Fossorial), and used the newly generated topology to estimate the states at the ancestral nodes for both characters. Different from all previous studies our phylogenetic analyses retrieved a highly supported phylogenetic hypothesis for the evolution of this endemic radiation. The genus *Grandidieria* was consistently recovered as the sister group of the clade comprising the genera *Flexiseps*, *Voeltzkowia*, *Pygomeles*, *Amphiglossus* and *Brachyseps* and we identify a candidate new genus. The ancestral state reconstruction suggested that five clades have independently evolved toward snake-like forms from fully quadrupedal and pentadactyl ancestors, while the biogeographic analysis suggested that the moist forest of the eastern coast likely played an important role in skink diversification.

Keywords: biogeography, Madagascar, molecular systematics, phenotypic evolution, skinks

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*Speaker

Heritability and evolvability of morphological traits of the honeybee *Apis mellifera* in tropical islands from the Mascarene archipelago

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Before invoking evolutionary process to explain morphological divergences among insular populations, estimation of morphological heratibility is essential. Indeed, phenotypic divergence between populations could be the result of either phenotypic plasticity or micro-evolutionary response to contrasted environments. A given phenotypic trait could evolve only if it could be transmitted to the next generation, i.e. it has a genetic basis. Quantitative genetic studies typically permit to estimate this part of the genetic variance in the phenotypic variation of a trait, this ratio is the heritability. The islands and archipelagoes of the Southwest Indian Ocean (SOOI) present a great diversity of habitats. As evolutionary forces are exacerbated in islands, populations are expected to show large divergence between islands. Several studies have demonstrated genetic and morphological differentiation between populations of the honeybee *Apis mellifera unicolor* in the SOOI area. Hybridizations between African and European lines, introduced by beekeepers in La Réunion and Mauritius, may explain a part of this differentiation pattern. *Apis mellifera unicolor* is an eusocial species with a polyandric and monogynic reproduction regime allowing quantitative genetic study to be conducted from wild populations. The objective of this study is to improve our understanding of the phenotypic differentiation of *Apis mellifera unicolor* populations in Reunion and Mauritius through heritability estimates of two morphological characters. We will assess the heritability of the size of the wings and the length of the proboscis, two traits subjected to different evolutionary forces. We sampled 6 colonies in Reunion Island and 8 colonies in Mauritius, with 95 workers per colony. All individuals were genotyped using 8 microsatellite markers to reconstitute the pedigree of each colony. Morphometric measurements on individuals with known degrees of relatedness will allow to estimate the heritability of these traits, using a so-called animal model.

Keywords: *Apis mellifera*, heritability, La Réunion, Mauritius, morphometry

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Interdisciplinary Island Studies

Contents

First mapping of water quality in Glorieuses archipelago : What monitoring strategies should be adopted?

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The Glorieuses archipelago, located north of the Mozambique Canal, is composed of two tiny islands on a reef complex of 196km^2. No bio-physico-chemical monitoring of water quality has ever been carried out in this pristine environment. The aim of this study is to establish an initial mapping of the quality of the archipelago's waters, enabling long term monitoring strategies to be proposed in order to have better management of this area. Physical-chemical parameters in the water and sediment matrix were acquired, initial status of chemical contaminants for water and sediment matrices were developped, data on the patterning of the water column to help understand habitat distribution were collected and data on soft substrate benthos as an indicator of marine environmental quality were collected. The bio-physico-chemical parameters of the water column show a very high homogeneity between stations and seasons. Glorieuses waters are (ultra)oligotrophic. Phytoplankton communities are characteristic of tropical environments, dominated by picoplankton and the microplankton dominated by diatom assemblages Chemical contaminants are almost absent with only 6 molecules exceeding detection limits. The hydrological parameters along the water column are also very homogeneous, indicating a significant mixing of water masses. The phyisco-chemical parameters of sediments are also very homogeneous between stations with poor organic matter concentration. Likewise for the benthic macrofauna. Despite the high homogeneity of water quality data, it is possible to identify 3 sectors with different characteristics. NNW Grande Glorieuse: waters richer in nutrients and (Pico)phytoplankton with sediments richer in organisms. Downwind area enjoying an "island effect" for water enrichment. Reef band between the two islands : coral shoal with strong hydrodynamism and therefore a significant mixing of the waters leading to poorer population of benthic organisms and low concentrations of nutrients and phytoplankton pigments. North : Deeper and populated by marine phanerogams, the water quality is very homogeneous. In addition, benthic communities that are also highly homogeneous indicate a classical oceanic influence. Based on these results and conclusions, management recommendations are made in the selection of sampling stations by sectors, lists of parameters and sampling periods.

Keywords: water quality, phytoplankton, Glorieuse

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Teaching Island Biology, and now also, Island Sustainability

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Teaching Island Biology at the undergraduate level at the Gump Station on Moorea, French Polynesia, has illustrated much about instruction of island biology and teaching field courses. Lessons include the importance of active learning, discovery experiences, local collaborations, and interactions of cultures. Challenges include dealing with remote locations, ensuring health and safety, and equity, inclusion and diversity. In addition to unique and fascination biology, islands are microcosms for environmental concerns, including climate change, sea level rise, changes in land use, invasive species, emerging diseases, and access to fresh water, among others. With this in mind, we have developed a new course in Island Sustainability, that will be taught through the University of California Education Abroad Programs (EAP), for the first time Winter/Spring 2020. Here, we hope to exchange course outlines and materials, as well as big ideas and best practices. Island Biology and Geomorphology (http://www.moorea-ucb.org/) is a popular course taught by professors and teaching assistants from University of California Berkeley. For 9 weeks in the Fall semester, 22-25 students live at the Gump Station. Following introductory field trips on Moorea and nearby Tahiti, students develop independent projects on all elements of the island's biota, including marine and terrestrial systems. Students learn by assisting others with projects and then present in a symposium at the end of the semester, which is published in an annual class book and on-line. Students frequently work with local institutions, including an agricultural college, beach-side hotels, and the Atitia Cultural Center. Students receive training in health and safety. While the course is incredibly popular, women applicants continue to far outnumber men. Island Sustainability (http://eap.ucop.edu/OurPrograms/french_polynesia/Pages/island_sustainability.aspx/) is designed to complement Island Biology, and use Moorea and neighboring islands of Tahiti and Tetiaroa, as a platform to provide training in environmental sustainability and resilience. The course will emphasize the local context of environmental solutions, including coral reef, marine, and terrestrial resources, cultural interactions, science communication, and advances in data science. The course is advertised through UC's Education Abroad Program and will coordinate with the University of French Polynesia.

Keywords: teaching, outreach, instruction, sustainability, resilience

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Homisland-IO: a homogeneous land cover over the small islands of the Indian Ocean

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The southwestern Indian Ocean comprises numerous islands of less than 3000 sq km (Comoros, Seychelles, Mascarene Islands). These small island territories have very fragmented and diversified landscapes. Satellite imagery and landcover products at low and medium spatial resolution (usually from 4 kilometers to 250 meters) are not or poorly suited to the study of these areas. Therefore, we have developed a land use product, called Homisland-IO, based on the analysis of high spatial resolution images acquired by the SPOT 5 satellite between December 2012 and July 2014 and produced at the SEAS-OI Station. We used an object-based image analysis method to identify the 11 major classes of land cover / land use of these tropical islands. This methodology together with a good knowledge of the field has enabled us to achieve an overall accuracy of 86%, making it an operational product. These products have already been used in various projects, including epidemiology and health geography (Lept-OI, TROI, ISSE-Mayotte, etc) to describe the distribution and habitat of some vectors of diseases (mainly mosquitoes and rodents), a necessary condition for analyzing the risk of transmission of these diseases to humans. Homisland-IO is freely accessible through a web portal and thus available for future uses.

Keywords: land cover, remote sensing, object, based image analysis, small island, Indian Ocean

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Collaborative and effective whale conservation in the Western Indian Ocean through soft law

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Most species of baleen whales were affected by important overexploitation by commercial whaling during the last century. They are nowadays concerned by numerous anthropogenic threats (*e.g.*, ship strikes, entanglement). As a result, many populations are reduced to small parts of their original sizes. Considering the humpback whale migration in the Western Indian Ocean (WIO), related economic benefits and the need to protect whales during their journey, a fisrt mandatory step towards whale conservation is to identify existing legal tools in the region. The protection of whales reveals a multitude of legal and institutional frameworks, or "regimes". Certain uses are then regulated like trade, or whaling. In addition, sanctuaries are established to ensure the tranquility of these great mammals from whaling like the Indian Ocean Sanctuary. At the national scale, marine protected areas are one of the most interesting legal tools for whale protection and conservation. Indeed, some marine protected area categories display operational regulations which can improve whale conservation but need to meet particular conditions to be effective. However, these international and national hard laws (or binding laws) reflect a fragmented landscape by the multitude of existing norms and by unequal involvment of States to protect whales. Thus, focussing on other tools to protect whales in the region is necessary. Indeed, legal frameworks are also supplemented by soft law, generating incitative commitments, often developed in the context of local characteristics. This applies, for example, to whale-watching charters or labels awarded to companies for their responsible whale-watching. Soft law can also lead to the creation of an Important Marine Mammal Area which is currently under way for the region. Considering the different tools implemented in the region and their effectivness, it appears that soft law plays a major role in the protection of whales. It also reveals that the protection of whales is a global phenomenon. This feature requires to exceed considering a specific legal order, either international, eitheir regional or national to favor an ecological approach.

Keywords: cooperation, humpback whale, label, regional protection, soft law, watching charter, whale, whale route

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*Speaker

Marine Ecology

Contents

Patterns and drivers of coral reef resilience at Aldabra atoll (Seychelles)

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The recent global coral bleaching event in 2016 caused mass mortality of corals worldwide and affected even the best protected and most remote reefs. This challenges the common notion that reefs far removed from local human impacts are more resilient to the effects of climate change. Remote islands and atolls offer the chance to better understand reef resilience under the exclusive influence of climate change. We studied the susceptibility to, and recovery since, the 2016 global bleaching event at Aldabra atoll, a remote UNESCO World Heritage site in the Western Indian Ocean. We combined the annual long-term monitoring of benthic and fish assemblages with additional observations of coral larvae settlement, and turf algae height at 12 permanent sites to assess post-bleaching trajectories (i.e. stability/recovery/degradation) and how these differ on an atoll-wide scale. Aldabra lost 50% of its hard corals during the 2016 bleaching event and experienced reductions of taxonomic and morphological diversity within the benthic assemblages. Initial results reveal location-specific diverging post-bleaching trajectories, with easterly reefs indicating further reductions in hard coral cover and increasing cover of calcifying and fleshy macroalgae. At the remaining sites, hard coral cover remained stable or increased, and turf algae cover decreased to pre-bleaching levels. Additional observations indicate atoll-wide similarities in turf algae height but marked differences in the density of settled coral larvae, which was substantially higher within Aldabra's lagoon. These results suggest that prevailing environmental conditions at individual reefs around the atoll are important drivers of reef resilience. Our results contribute to the understanding of the natural drivers of coral reef resilience at remote islands and atolls, thereby aiding the prioritisation of areas for conservation.

Keywords: coral bleaching, climate change, recovery, marine monitoring, remote

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Why is fine-scale thermal structure the key to the foraging success of little penguins?

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Phillip Island hosts a mega-colony of little penguins (*Eudyptula minor*), making them good bio-indicator of the marine ecosystem in Bass Strait, Australia. Little penguins forage better, increasing their prey encounter when a thermocline is present in the water column. It seems to act as a barrier for the prey, making them easy targets for the penguins. But they are dynamic structure in space and time, tending to get mixed and disappear under stormy conditions. In parallel, there are marked individual differences in the rate of prey encounter by little penguins. We thus hypothesized that daily differences in foraging strategies of individual penguins could reflect water column disturbance in their foraging zone. To evaluate this, we combined satellite oceanography and little penguin tracking data (n=20 birds) during the chick guard stage in 2018, a season of low reproductive success. We observed short-term water column perturbations during this period and, as predicted, penguins' foraging performances was substantially affected. We found an increase in distance travelled from the colony almost three times the average distance when feeding chicks. It was concurrent to a decrease in dive duration, depth, and prey encounter rates when the water column was more mixed. This change was accompanied by a deterioration of the body mass difference between and after a trip. Prey may have become more widely dispersed in the water column making them challenging targets for penguins. Mixed waters regimes are expected to become more frequent due to more stormy days under climate change. Our findings are crucial to predict the foraging success of little penguins accurately under less successful years to support fine-scale planning.

Keywords: foraging ecology, thermocline variability, GPS tracking, diving behaviour, Eudyptula minor

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Depredation mitigation device for pelagic longline fisheries: the PARADEP project

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Depredation in marine systems is defined as the damage or removal of fish or bait from fishing gear by predators. The long term objective of the PARADEP project is to reduce toothed whale depredation impacting pelagic longline fisheries (PLFs). This general objective comes in several components including scientific research, capacity building, communication and economic study. The scientific objective of PARADEP includes two sub-objectives. The first one is to develop a physical depredation mitigation device for PLFs targeting swordfish and tuna. This innovative device will have three protective skills: a physical protection (physical barrier between the fish and the predator), a visual protection (hiding of the fish) and a passive acoustic protection (modification of the fish acoustic signature). It will be tested in Reunion Island on board commercial pelagic longliners. The second sub-objective is to acoustically monitor the depredation process. Hydrophones and accelerometers will be deployed on the fishing gear along with the devices. This will allow to detect toothed whale presence in the vicinity of the longline, identify the involved species and analyze their acoustic behavior when they interact (or not) with the devices. The capacity building objective of PARADEP is to enlarge the research community working on mitigation of negative interactions between marine mammals and fisheries. This will include workshops organization and supervision of interns. The communication objective of PARADEP is to share the resulting knowledge to the public, political managers, stakeholders, scientists and fishermen. This will be done by the construction of a dedicated website and the participation to workshops, conferences and meetings. The last objective of PARADEP is to economically assess the loss due to toothed whale depredation impacting the PLFs of Reunion Island. This will allow to assess the position of the device in the market of fisheries equipment, based on its price. PARADEP is funded by the European Funds for Maritime Affairs and Fisheries (FEAMP), and is due to last 30 months (July 2018 – December 2020). It involves three partners: two French research labs (IRD MARBEC and CEBC CNRS) and one pelagic longline fishing company (ENEZ DU, based in Reunion Island).

Keywords: negative interaction, toothed whales, tuna, swordfish, physical device

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Physical and biological drivers of herbivory on subtidal reefs of tropical oceanic islands

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Shallow reef ecosystems on oceanic islands often present physical and biological conditions that have no analog to native ranges found on the mainland. It is unclear how species colonizing from the mainland function in these ecologically novel habitats. We evaluated the ecological impact of herbivorous fishes and urchins on subtidal rocky reefs in the Galápagos Islands, comparing their impacts to those on other tropical reefs and testing their response to variation in sea surface temperature and wave exposure. We found that fish herbivory is limited by food availability and is negatively correlated with temperature, whereas urchin herbivory is limited by wave exposure and is positively correlated with temperature. Fish feeding exceeds 120,000 bites/m2/day but does not fully remove algal thalli, maintaining low biomass but high diversity. Urchin densities surpass 59 urchins/m2, resulting in urchin barrens dominated by crustose coralline algae. Extremely high densities in their island range and the lack of reef building corals that might replace grazed algae changes the ecological context of marine herbivores in the Galapagos relative to their mainland counterparts. Additionally, we compared fish feeding capabilities at wave-induced flow speeds ranging from 0 to > 100 cm/s. Flow-adapted species from several families including Labridae, Pomacentridae, and Blenniida*e* tend to feed during calm periods in between high wave sets. Other herbivorous fishes such as *Prionurus laticlavius* and *Microspathadon dorsalis* showed feeding patterns spread across the entire range of flow, and seemed to prefer feeding at slightly higher wave flows (_˜27cm/s).These data suggest that variation in wave exposure and sea surface temperature may limit feeding for some marine herbivore species but facilitate it for others. Complementary ecological function among species that vary in their tolerance for environmental variation may serve to buffer marine ecosystems on oceanic islands from climate change.

Keywords: ecosystem functioning, environmental stress, Herbivory, hydrodynamics, reef fish

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Does global change enhance jellyfish population over the Reunion Island coral reefs? A comparison between 2006 and 2017

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Concern over a potential increase in frequency of Jellyfish blooms and their importance worldwide has rose over the past decades. Although jellyfish populations exhibit natural variation due to their complex life cycle and the environmental conditions, this phenomenon is certainly enhanced by human activities (overfishing, agriculture, coastal development), and their consequences on marine ecosystems (pollution, eutrophication, climate change). Unfortunately, jellyfish blooms can lead to several negative ecological and socio-economical issues. They can notably decrease fish populations, clog fishing nets, sting swimmers, and block water-cooling systems. A year-round sampling of plankton over Reunion island's coral reefs (South West Indian Ocean - 21◦S, 55◦E) was conducted in 2005-2006 and led to the identification of about 65 jellyfish species (Hydrozoans mostly). Species richness, seasonality and abundance of jellyfish were recorded twice a month, using vertical tows from 8 stations. A second assessment started in January 2017 following the same protocols and sampling grid during 8 months. The aim of the present study is (1) to compare the jellyfish community structure and their spatiotemporal variability, over a 10-year period and (2) to evaluate the potential relationships with global change. The species richness was similar in 2006 and 2017, with a large predominance of hydroidomedusae. Both years, the automedusae (narcomedusae and trachymedusae) showed a very low number of species but were very abundant in all sites. The Cubomedusae *Carybdea* sp. (a jelly-box caught in 2006) was still present in Reunion marine water in 2017 but, fortunately, do not present a lethal risk to humans. The total jellyfish abundance showed significant differences between the 2 years investigated, with more specimens in 2006 than in 2017. The better Shannon indexes calculated for 2017 could parallel the MPA establishment in the west coast of Reunion Island, since 2007. Monitoring should continue, especially in austral summer when jellyfish abundances are the highest and swimmers numerous, in order to gather more information on the jelly community in this South-western Indian Ocean tropical area, where a lack of knowledge on this marine compartment is particularly evident.

Keywords: abundance, global change, jellyfish biodiversity, marine monitoring, MPA

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Does climate change affect coral and hydroids reproduction? 10 years of monitoring in fire and scleractinian corals in Réunion island

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Coral reef health is linked to the reproductive capacity of reef building corals that may be impaired by global warming and repetitive bleaching events. Monitoring the sexual reproduction and the larval settlement in these corals might help the managers for MPA planning. Here, we monitored the reproductive effort of the fire coral *Millepora exaesa* and the larval settlement of scleractinians on artificial tiles over 10 years, on the reef flats of Reunion Island. Two study sites were selected, a highly frequented (B) and a human-preserved site with more oceanic influence (K). During the austral summer, the rate of reproducing fire coral colonies and the density of their ampullae (reproductive features) were measured. The larval settlement of scleractinians was counted on tiles immerged before coral spawning and collected 6 months later at the end of the reproductive season. At the beginning of the monitoring, 60 to 80% of the fire coral colonies showed ampullae on the coenosteum surface at the 2 study sites with a similar ampullae density. This rate falls down to 20% in K, 8 years later, while it remains the same in B. The same trend was noticed for scleractinian larval recruitment with a drastic decrease in the number of recruits on the K tiles over the 10 years of monitoring and the replacement of acroporid recruits by pocilloporids. These results were surprising as this study site was expected to be less subjected to increase temperature because of its oceanic influence and to human impact due to its remote position. Yet these trends may be explained by the increasing quantity of sediment flowing down from the K watershed that may have reduce the fitness of coral colonies. For the last 10 years, numerous buildings, roads and rainproof platforms were constructed on the slope of the watershed enhancing soil leaching and bad water quality on the reef flats. We hypothesised that decrease in reproductive effort and recruitment rate are linked to the uncontrolled urbanisation on the watershed leading to increase turbidity and degraded water quality. This perturbation is strongly decreasing the chance for coral to cope with global warming.

Keywords: monitoring, climate change, coral reproduction, coral recruitment, long, term series

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Genomics of adaptation on islands

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Whole genome sequencing projects can have a major relevance in understanding health, genetic disease, species adaptive evolution and molecular diversification. Currently, multiple species are having their genomes completely sequenced, from simple organisms, such as bacteria (e.g. microbiomes), to more complex taxa, such as higher vertebrates. This voluminous sequencing data generated across multiple organisms provides also the framework to better understand the genetic uniqueness of such species and related ones, allowing to explore the genetic changes underlining the evolution of diverse phenotypic and adaptive traits in species inhabiting marine islands. Here, recent results retrieved from comparative evolutionary genomic analyses of various endemic animal species living in marine islands (e.g. terrestrial mammals, birds, reptiles, marine snails) will be considered to exemplify the adaptive success of species (e.g. venom diversification, innovative phenotypic traits) into diverse islands environments and lifestyles. The findings pinpoint unique molecular products of critical relevance in species evolution, diversification and conservation, but also highlight genomic novelties (e.g. venom compounds) of importance for environmental and biomedical research.

Keywords: adaptation, animals, evolution, genomics, islands

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Negative impacts of drifting FADs in the EEZ of French Polynesia

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In 2019, the major concern of Regional Fisheries Management Organizations (RFMOs) in the 3 oceans is the very large use of drifting fish aggregating devices (FADs) for the exploitation of large pelagic fish (tuna and related species) by the purse seine fleets. The most reasonable estimates indicate that more than 100,000 of these gears would be permanently deployed at the surface of the tropical oceans. Beyond the risks of major overexploitation of the main targeted species, this technique induces an unbalanced competition between industrial fishing and artisanal fisheries, leading to a strong depletion of resources available for these small fisheries. It also generates large discards and numerous bycatch of emblematic and vulnerable species such as turtles and sharks. Drifting FADs also represent a real danger for shipping and a major source of pollution since they inevitably end their lives, either on the bottom of the oceans or beached on the coasts. Although purse seine fishing and the use of drifting FADs are prohibited in its EEZ, French Polynesia is threatened by the consequences of this situation. Indeed, French Polynesia is bordered by two of the largest drifting FAD fishing areas on the planet, the Eastern Pacific Ocean (EPO) to the east, and the WCPO (Western and Central Pacific Ocean) to the east. Its large EEZ is regularly impacted by FADs released in these two fishing grounds that generate problems including growing complaints from local fishermen and island populations. Researchers (UMR EIO, GEPASUD) have teamed up with the managers of the Marine Resources Department of French Polynesia (DRM), to characterize and quantify the consequences of the massive influx of drifting FADs crossing the EEZ. The methodology used is based on the combination of oceanic drift modeling of these devices and field surveys involving scientists and a network of observer fishermen. These data should enable us to obtain a first quantified assessment of the damage suffered by the Polynesian fisheries from these large foreign industrial fleets.

Keywords: FAD, fisheries, Pacific ocean

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Influence of post-settlement events on coral population structure: a multi-scale analysis along a latitudinal gradient

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Scleractinian coral communities often show strong dissimilarities between settlement patterns and the distribution and abundance of adult corals. The relative contribution of post-settlement events (e.g. competition, predation, facilitation and disturbances) on the structure of adult populations is still unclear. The purpose of this study is to assess the importance of post-settlement mortality, retention, positive and negative growth in determining the spatial patterns and abundance of adult corals with different of life history traits (e.g. *Acropora*, *Pocillopora* and *Porites*). Surveys were conducted along a latitudinal gradient, with three islands: Orpheus Island on the Great Barrier Reef (GBR), Grande-Terre, in New Caledonia, and Moorea in French Polynesia. On each island, two sites were defined and three habitats per sites were studied: the inner reef (¡ 2 m depth), the shallow outer reef slope (¿ 6 m) and the deep outer reef slope (¿ 15 m). At each of these 18 stations, the first thirty colonies were sampled and were monitored and measured three times at six months apart: t0, t1 (6 months) and t2 (12months). Overall, the young coral mortality is weaker in Grande-Terre (35.3%) than Lizard Island (44.7%) and Moorea (60.2%). These mortality rates are similar among the three coral taxa, and did not show significant difference among habitat. The linear growth is higher in Lizard Island (16.0 mm.y-1) and Moorea (14.1 mm.y-1) than Grande Terre (5.0 mm.y-1), and higher for *Acropora* (16.0 mm.y-1) and *Pocillopora* (14.5 mm.y-1) than *Porites* (4.6 mm.y-1). Overall, demographic processes are dominated by mortality, retention and positive growth, whereas negative growth is less important. This study shows the seasonal variation of young coral demographic processes and the interannual variation especially at Moorea after cyclone Oli which has greatly decreased survival and linear growth at different scales. This study shows a more dynamic ecosystem in Moorea than Lizard Island and Grande Terre. Coral communities of Lizard Island and Grande Terre present a same structure (abundance and size class) but a different of dynamics. To conclude, most of demographic processes are governed by particular environmental conditions at biogeographic, insular and local scales of studies.

Keywords: coral reef, juvenile coral, multiscale analysis, population dynamics, post settlement events

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Phenology, at-sea distribution and activity of a critically endangered tropical seabird, the Mascarene petrel (*Pseudobulweria aterrima*)

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Mascarene petrel (*Pseudobulweria aterrima*) is a critically endangered seabird endemic to Reunion Island. The population size is between 50 and 100 pairs and the species is impacted by several anthropogenic threats, such as introduced mammals and light pollution. Two breeding colonies were discovered in 2016-2017, which allowed the first extensive research on its ecology and biology. Our study aimed to determine, for the first time, phenology, at-sea distribution and activity patterns of Mascarene petrels thanks to GeoLocator Sensors (GLS). 23 GLS were deployed in 2017 and 14 provided data after one year. These GLS showed that their at-sea distribution is very large, covering a large part of the tropical Indian Ocean. When breeding, they forage in the western Indian Ocean around Reunion Island, and after breeding, birds performe a large scale migration. In contrast to Barau's petrel, the other endemic petrel from Reunion Island, Mascarene petrels migrate in various oceanic areas of the Indian Ocean. They use mainly five wintering areas : south of Sri Lanka (n=2), Arabian Sea (n=4), Bay of Bengal (n=2), Mascarene and Seychelles plateaus (n=5) and west of Australia (n=1). This huge heterogeneity in wintering areas was not related to sex. At-sea activity of Mascarene petrels revealed that they spent on average 34.1% (±5.43) of their time in contact with seawater, and more precisely 8.6 hours/day (±1.15) on foraging, 5.5 (±0.88) on floating and 12.0 (±1.67) on flight. All these behaviours are significantly different according to the photoperiod and breeding season. Indeed, during the breeding period they spent on average 15.2% of their time in contact with seawater, 53.0% during the non-breeding, 24.3% during the night and 46.7% during the day. At night, at-sea activity patterns were strongly correlated to moon phases, birds exhibiting a lower percentage of time spent on water during full moons. The annual phenology of each bird has been defined by combining light, geolocation and conductivity data. All these results will be very useful to evaluate the species vulnerability during their marine phase and to develop appropriate conservation strategies.

Keywords: at sea activity, conservation, endangered species, migration, seabird

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A shark Reunion: environmental DNA assessment of an oceanic island

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Reunion Island is an oceanic island 800 km east of Madagascar, which is the closest large landmass. Such isolation may promote faunal divergence and reduced colonisation from many marine species that inhabit coastal habitats. Yet, remote islands may also serve as natural ‘oases’ for the conservation of species that are vulnerable to the impact of human activities. Elasmobranchs (sharks, rays and skates) are an important component of marine ecosystems, and are globally threatened by overexploitation and habitat degradation. Elasmobranch diversity in Reunion Island is poorly understood, but recent observations suggest that several species once common, such as reef sharks (*Carcharhinus melanopterus*, *Trianodon obesus...*) may have disappeared in the past few decades, due to overexploitation. Here, we assessed elasmobranch diversity around Reunion Island by retrieving trace DNA fragments from 114 sea water samples collected at 16 sites and two depths (10 and 40 m), with a temporal replication of sampling at least every 15 days – an approach known as ”environmental DNA (eDNA)”. Samples were screened using DNA metabarcoding, targeting a 182 bp fragment of the 12S mitochondrial DNA, specifically designed for elasmobranchs. Results are discussed in the context of environmental conditions and habitat types between the east and the west coasts of the island, in order to better understand the mechanisms affecting elasmobranch diversity in this remote oceanic island. By comparing biodiversity records detected through eDNA with published species lists from Reunion Island, we discuss advantages and limitations of the eDNA approach, and appraise its present and future application in monitoring shark biodiversity.

Keywords: biodiversity, elasmobranch, environmental DNA, metabarcoding, Reunion island

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Palaeo-biology / Palaeo-environments

Contents

Reconstructing past vegetation cover on the Azores using pollen-based models

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Many oceanic islands have undergone dramatic ecological changes during the last few centuries. Human activities and exotic species have so greatly modified the landscapes of these islands that the original vegetation is difficult to imagine. Areas of remnant vegetation are therefore used as baselines for restoration. But how representative are these remnants of the original vegetation? In this contribution, we use pollen-based modelling to provide quantitative reconstructions of past vegetation cover on the Azores. We combined pollen and vegetation data from 24 sites on Ilha das Flores to produce pollen productivity estimates for key Azorean plant taxa and then applied these to fossil pollen records. The results indicate that some remnants where *Sphagnum* mosses now dominate had quite different vegetation composition prior to human arrival. Restoration goals and species distribution models for the Azores may be improved using pollen-based reconstructions of past species abundance, distribution and dynamics in the recent past.

Keywords: modelling, oceanic islands, palaeoecology, restoration, vegetation

Sphagnum overgrowing remnant *Juniperus brevifolia* stands, Ilha das Flores, Azores (photo: S. Connor)

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Paleoecological changes in Lake Funda (Flores Island, Azores): tracking human impacts in a remote island lake throughout the past millennium

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Previous studies on lacustrine sedimentary sequences in the Azores show that climate variability and vulcanism along with the arrival of humans played a significant role in the recent development of these insular Azorean ecosystems. However, the timing and rate of anthropogenic impacts on these lakes is poorly constrained. Paleoecological research allows us to reconstruct ecological conditions prior to and after human settlement, thereby contributing to our understanding of how species and island ecosystems responded to both natural and anthropogenic disturbances. To assess both types of impacts over the last 1000 years, we analysed the elemental geochemistry on bulk organic matter, diatoms, and chironomid remains in a 994 cm-long sediment core recovered from Lake Funda (Flores Island, Azores) in 2017. Preliminary results from Lake Funda show that human colonization was the main driver of ecological changes. We identified three major ecological phases: (1) 950-1350 yr AD, a pristine lake ecosystem with mesotrophic diatom taxa, including benthic and tychoplanktonic life-forms, and free-living chironomids species representing an undisturbed environment; 2) 1350-1450 yr AD, the release of cattle and gradual forest clearance lead to an increase in nutrient inputs and the start of the human-impacted phase; and, (3) after Portuguese settlement, from 1450 yr AD to present, a second human-impacted phase resulted in lake eutrophication and the development of an anoxic hypolimnion due to an increase of nutrient loading. The first anthropogenic phase resulted in a drastic 50% decline of the overall biodiversity with a shift to planktonic diatom species and free-living chironomids, while the second was characterised by a substantial reduction in the density of chironomids and diatom assemblage shifts towards the dominance of *Aulacoseira granulata* and *A. ambigua* suggesting a shift in lake trophy. Other external drivers like major climate oscillations likely play a role within these phases as well. Our study demonstrates the sensitivity of aquatic ecosystems in remote islands to anthropogenic impacts that have the ability to overtake natural forces of variability (i.e., climate).

Keywords: Environmental reconstruction, diatoms, chironomids, early human impacts, remote islands

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To what extent is the current spatial distribution of organisms shaped by past environmental dynamics?

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During the late Quaternary, climatic oscillations have resulted in major fluctuations in sea level and, correspondingly, changes in island area and isolation. We quantified sea-level driven changes in paleogeography of 178 islands worldwide and stored these new data in the Palaeo-Island and Archipelago Configuration (PIAC) database. We used these data to assess the role of past archipelago configurations in shaping the present-day distribution of endemic land snails and angiosperms. This was done by fitting linear mixed models for different archipelago configurations using the number of endemic and (non-endemic) native species as a response. Our online database shows that oceanic islands are dynamic entities: they emerge and submerge; they shrink and expand; they split and merge. The data also underlines that the present-day situation is exceptional: for most of the late Quaternary, islands were larger than today, and less isolated. Consistent across both studied groups, we found that patterns of single-island endemic species in particular are related with past environmental dynamics. Long-lasting

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*Speaker

configurations have left a stronger imprint on their distribution than extreme archipelago configurations that persisted for a few thousand years only. To understand the spatial distribution of island biota it is therefore essential to consider longer-lasting past environmental conditions, rather than the current situation alone.

Keywords: endemism, glacial–interglacial cycles, late Quaternary, past environmental change, sea-level oscillations

Restoration Ecology / Ecological Restoration

Contents

Natural recruitment of *Scalesia pedunculata* on Galápagos after control of invasive plants

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The Galápagos islands comprise a unique flora with high percentages of endemic species. At the same time, the number of non-native plant species present on the islands currently exceeds the number of native and endemic species. These introduced plants have altered vegetation and ecosystems throughout the archipelago. The Scalesia forest on Santa Cruz, naturally dominated by the endemic and eponymous tree species *Scalesia pedunculata*, is currently being transformed by invasive plant species such as the introduced blackberry *Rubus niveus*. In a trial area within the remnant Scalesia forest, invasive tree and shrub species have been removed for restoration purposes. There we studied the natural recruitment of *Scalesia pedunculata* after invasive plant species control. Data suggest that seedling survival of *Scalesia pedunculata* is mainly driven by light availability. Our results illuminate the impact of invasive species on forest recruitment and corroborate the importance of precisely distinguishing between the effects of discrete non-native plant species on ecosystems that are to be restored.

Keywords: restoration, invasive, Scalesia, Galápagos, natural recruitment

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Monitoring an endemic thermophilus woodland reforestation in Tenerife, Canary Islands

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The thermophilus woodlands in the Canary Islands are among the most endangered ecosystems due to human exploitation over the last five centuries, especially on the largest and most populated island, Tenerife. The Canarian juniper woodland dominated by *Juniperus turbinata* ssp. *canariensis*, is included as a priority habitat in the Directive 92/43/EEC (9560). As a result, a reforestation project (LIFE04/NAT/ES/000064) was funded by the European Union from 2005 to 2008 to recover the Rural Park of Teno, which harbour one of the last remnants of thermophilus woodland on Tenerife. To assess the ecosystem response after the reforestation, two monitoring processes were carried out: the first one from 2005 to 2008 and the present study based in the period between 2014 and 2018. We recorded the vitality, the phenology and the growth traits (height, stem diameters and crown diameters) of 225 planted individuals belonging to 8 different species inside 6 fixed plots, in each spring from 2014 to 2018. We analysed the temporal variation of the recorded variables. Furthermore, we tested the two dominant species (*Juniperus turbinata* ssp. *canariensis* and *Olea cerasiformis*) among the plots to verify any variation in local growth patterns. The vitality and the phenology showed general positive trends, despite a decrease in 2018. Only the two dominant species presented a significant p value for all the growth traits. The juniper showed local patterns of growth and was more influenced by local conditions than the wild-olive, which responded evenly. Some invasive species are recolonizing the estate, so actions are needed to control them. In short, the monitoring proved to be useful to quantitatively evaluate the reforestation effort.

Keywords: ecological monitoring, restoration ecology, Canary endemic juniper community, functional traits

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Let the problem become the solution: using cost-effective, holistic ecological and horticultural approaches to conserving St Helena's rare cloud forest ecosystem

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Saint Helena, a _˜14-million-year-old island in the South Atlantic Ocean, has endured extreme anthropogenic pressures over the 517 years since its discovery, leading to severely diminished and fragmented native habitat. Although remaining native habitat on Saint Helena makes up less than 1% of the total land area, most of which is confined to cloud forests located at the highest elevations of the island, it contains close to 30% of the total endemic diversity of the UK and its overseas territories. Four endangered keystone endemic tree species of the native cloud forest are in decline, with the remaining populations of each species having been reduced to lone trees or small groups.

Our ongoing project aims to secure the survival of these four tree species and their associated invertebrate fauna. We obtained clonal material from all known remaining individuals of each species, multiplied these ex-situ and placed them in species-diverse genetic field gene banks adjacent to native habitat fragments to function as habitat restoration plantings. By placing gene banks adjacent to native habitat, native invertebrates naturally migrated into these sites, both above and below ground, with benefits to ecosystem function. By sampling clonal material from the entire pool of individuals of each species (rather than selecting individuals based on phenotype, ease of accessibility, or horticultural preference) and placing them in close proximity to one another, gene flow improves, leading to increased genetic variability in subsequent generations.

Movement of native invertebrates between sites will be further facilitated through outplanting of genetic stock raised from the field gene banks, with the aim of increasing the linkages among self-sustaining native ecosystems, creating corridors between habitat fragments by replacing invasive species with natives. The ecological and horticultural techniques employed in this project use relatively few resources but have already yielded demonstrable successes in increasing the local genetic diversity of endemic plants and increasing the numbers of invertebrate fauna, and could be employed in other island systems.

Keywords: Habitat restoration, novel ecosystems, field gene bank, invasive species management

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Effects of habitat restoration on the seed dispersal ecosystem function in Seychelles

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One of the greatest threats to native island biodiversity are biotic invasions. Invasive species alter biological interactions, which can disturb key ecosystem functions such as seed dispersal, an important plant-animal mutualism for the regeneration of natural vegetation. In Seychelles, as in all other tropical regions, the majority of the woody plant species produce fleshy fruits, which require frugivores for dispersal. On many islands these processes have been substantially disrupted. Here, we ask whether plant-frugivore interactions can be restored by invasive alien plant removal, which is a common method in ecological restoration. Understanding the response of frugivores to restoration is critical to assess the potential of restoring plant communities on ecosystem functioning. We present seed dispersal interaction networks collected on eight inselberg plant communities in Mahé, Seychelles. To record plant-frugivore interactions and construct the seed dispersal networks we combined three different sampling methods: camera traps, observations, and faecal analysis. We used an established restoration community experiment to investigate the longer-term responses of the removal of exotic plant species on the seed dispersal mutualism. We will present results from a first field season and discuss the findings in the context of structural and functional changes of the plant-frugivore community as a response to restoration.

Keywords: ecological restoration, biodiversity conservation, interaction networks, seed dispersal, mutualistic interactions

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Invasive mammal eradication and seabird communities: Island recovery in the world's seabird biodiversity hotspot

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Islands support some of the greatest numbers of endemic species but are highly vulnerable to anthropogenic activities, including the introduction of invasive, predatory mammals. Mammal eradication is a primary conservation tool to protect island communities, yet little is understood about how communities reassemble and how assembly patterns influence island ecosystems. Seabird assemblages of many restored islands differ from their uninvaded counterparts due to variability in colonization rates and differences in important interactions between and among species. New Zealand – the world's largest seabird biodiversity hotspot – has eradicated mammalian predators from > 100 islands over many decades, providing a unique opportunity to quantify seabird community recovery. Here, we examined seabird community assemblages across New Zealand's outlying archipelagos, coastal, and near-shore islands in relation to island-specific histories of predatory mammal introductions and eradications. In a literature review, we collected data for seabird colony sizes located within New Zealand for 84 species belonging to the orders Sphenisciformes, Procellariiformes, Pelecaniformes, and Charadriiformes. To assess whether seabird communities were recovering on islands that have been cleared of invasive mammals with varying time since eradication, we used generalized linear mixed-effects models (GLMMs) to compare seabird community assemblages among islands that are uninvaded and currently invaded by mammalian predators. We found that seabird biodiversity initially increased in the years immediately following mammal eradication but gradually decreased over time, possibly as a result of competition during early recolonization. Our averaged-model predicted that seabird diversity at older restored islands ($\geq$15 years post-eradication) were similar to that of uninvaded islands. This demonstrates seabird communities are slowly recovering from mammalian invasions. Our results emphasize the need for monitoring programs that are vital for understanding community assembly processes on islands.

Keywords: Seabirds, island invasions, island restoration, community reassembly

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Providing knowledge about seed germination ecology to boost establishment success in revegetation projects: case study of *Heteropogon contortus*

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Dry lands including savannas cover an important proportion of terrestrial areas and are home for more than a third of global population. However, changes in land use and climate are causing severe species loss in these habitats. In a geographically limited area such as Reunion Island, revegetation projects including native species could allow to counter human-driven habitat degradation. Nevertheless, lack of knowledge, especially regarding native seed germination ecology often hinders their use for revegetation purposes. The aim of our study was to provide information about seed germination ecology of *Heteropogon contortus* (Poaceae), the dominant and noticeable savannas species of Reunion Island. Through germination experiments carried out in controlled lab conditions, dormancy and light requirements of *H. contortus* seeds were assessed over a 3-year storage period. In addition, the effects of smoke water solutions on *H. contortus* seeds germination capacity were determined. During the first year, seeds germinate in low proportions, consistent with a dormancy phenomenon. Moreover, between one and two years, germination percentages are higher in light than in darkness, suggesting they are photoblastic (i.e. require light for germination). Interestingly, seeds treated with smoke water solutions germinated in higher proportions than control seeds in both daily light and darkness during the two first years of storage. The germination strategies (dormancy and photoblasty) set up by *H. contortus* are likely driven by harsh conditions found in arid habitats such as savannas. While dormancy could help avoiding germination in the drier season, photoblasty would be linked to an adaptation to fire, indicating that its environment is suitable for its establishment. The methods we used to treat seeds could be adopted for large-scale *H. contortus* habitats revegetation projects, due to their low cost, their efficiency and their reproducibility.

Keywords: *Heteropogon contortus*, germination, physiological dormancy, photoblasty, smoke, infused water, revegetation

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Reproductive biology of *Phelsuma guentheri* (Reptilia: Gekkonidae) and the effects of habitat restoration on Round Island (Mauritius)

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With no introduced predators, Round Island was the sole refuge for many Mauritian species. However, introduced goats and rabbits had major negative effects on the island. Following their extirpation in 1986, the palm forest has regenerated well. In 2001 restoration planting of native hardwood forest began. Guenther's gecko, *Phelsuma guentheri*, formerly widespread in Mauritius, is today only found on Round Island and Ile aux Aigrettes. Round Island is home to an estimated 2,300 *P. guentheri* – below expectations for a large reptile inhabiting a palm-rich habitat. On Ile aux Aigrettes, *P. guentheri* frequently use hardwood trees as nesting sites; but large hardwood trees are still rare on Round Island. Hence nest-site limitation may limit the abundance of *P. guentheri* geckos across Round Island. We here report preliminary findings of an ongoing investigation of egg-laying behaviour, nest site availability and incubation conditions for *P. guentheri* on Round Island; with a special focus on the potential role of the restoration of hardwood plant species. We recorded and followed the fate of 1443 eggs across 269 nesting sites. The majority of these were on *Latania loddigesii* palms (212 sites), with rock sites being second (36 sites), and the remaining sites on other substrates. While palms were most often chosen as nesting sites, the rock sites held more eggs per site (mean: 13.75) than those on palms (mean: 3.88). By the end of the field season, 744 eggs had hatched, and 56 failed. Communal nesting occurred on all substrates, but most often on rock. Eggs were laid in the early evenings, whereas they hatched throughout the day. We failed to find the expected importance of hardwood plants as nesting sites for *P. guentheri* on Round Island, possibly because hardwood plants are still relatively sparse on Round Island and many saplings are still small. Alternatively, the observed nest-site use on Ile aux Aigrettes does not reflect a preference, but is caused by the relatively low number of adult palms and missing rock overhangs on this island. Future studies on Round Island, when both adult palm- and hardwood forests will be available, would address this.

Keywords: *Phelsuma guentheri*, island restoration, reproductive biology, species abundance, nest site selection

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Impact of collecting seeds from black-and-white Ruffed lemurs feces on natural regeneration at Kianjavato forest fragments, SE Madagascar

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The rates of germination success of seeds collected from the feces of animal dispersers, as well as seedling survival have been reported on in numerous previous studies. About a decade ago, seeds were extracted from the feces of *Varecia variegata* or Black-and-white Ruffed Lemur in the Kianjavato forest (KF), southeastern Madagascar, to supply tree nursery stock. KF includes several fragments of mid-altitude rainforest, where a reforestation program has been conducted since 2009. Successful seedlings from the nursery are planted to form corridors between each forest fragment (FF). However, no information is available on the impacts of these extractions on the natural regeneration rate (RR) of tree species. This study provides information of the potential impact of such collection activities on the RR of five tree species: *Canarium planifolium*, *Cryptocarya myristicoides*, *Norhonia urceolata*, *Uapaca ferruginea* and *U. thouarsii*. We conducted this study in four KF fragments, including two control fragments characterized by the absence of seed extraction from *Varecia* feces and two fragments where seeds are collected from lemur feces each month. The RR of the five target tree species in the two types of FF was compared based on young trees with basal diameter lower than 2.5 cm and within 10 m of the parent trees. Regeneration rate is higher for all five tree species in all FF where seed extraction was performed compared to those from control fragments. Our results demonstrate that seed extraction activities improve seedling survival and encourage noncompetitive growth. Collection of seeds contained in *Varecia* feces does not have a significant negative impact on the natural regeneration rate of the five target species in KFF. However, over time, these collections may have consequences on the regeneration of these species due to lower seed supply.

Keywords: Kianjavato forest, Madagascar, regeneration rate, seed collection, *Varecia variegata*

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Social Sciences on Islands

Contents

Ecological restoration of the tropical semi dry forest in Réunion island: exploring dimensions of ecological awareness

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Ecological restoration is a process of repairing the dynamic of an indigenous ecosystem damaged by human activities. In 2012, an ecological restoration program has been established in Reunion island, the aim of this project is to restore the tropical semi dry forest at *La Grande Chaloupe*, which represents -nowadays- only 1% of its original area. However, the project ends in 2020 and the endowment of the local environmental governance remains unclear. The main issue is the sustainability of ecological restoration actions by local people. For a better understanding, we explored the dimensions of ecological awareness of the population of Reunion island by applying a conceptual model of ecological awareness of this population. A random sample survey of 1,000 individuals was conducted in 2017 (between *Saint Denis* and La *Possession*) through a questionnaire survey, we analyzed the relationship between environmental concern, environmental knowledge and environmental behavior of the population of Reunion Island regarding the ecological restoration project of the tropical semi dry forest. Findings shows that about 20% of the population were aware of the existence of this project and confirm that there was a significant relationship between environmental knowledge and environmental concern. This conceptual model aims to be a tool to measure the resilience for a better understanding of the forests socio-ecological system and might be also as an indicator of ecological observations (e.g. the rate of alien species invasion).

Keywords: ecological awareness, ecological concern, ecological behavior, ecological knowledge, resilience

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The input of the Xth European Fund for Development (EFD) in capacity enforcement in Mayotte

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As part of the regional component of the Xth EFD, and its objectives of strengthening the knowledge of the marine environment and related activities, the Mayotte Marine National Park, has trained field agents in the techniques and protocols of observation of coastal fisheries on land and at sea. The Mayotte Marine National Park is the operator of the FIS (Fisheries Information System) which is a data collection program on professional fishing at the national scale. The FIS provides an overview of professional and subsistence fishing activities and bases management actions on solid knowledge of the sector. The FIS consists of collecting and gathering fishery data through fishermen surveys and observations. It's about sampling to take the measurements and identify the species. The protocols being standardized, these skills will be transferable on all the territories. The annual calendar of activity of a vessel is to indicate for each month of the year considered whether the ship was active or not, and if so, the list of trades. The embarked observer program is based on a sampling plan. It fixes for each observer the schedule of the landing sites to be frequented and the fleets to be surveyed. With the agreement of the fisherman, the observer counts or measures some of the catches of certain commercial species of major interest for the management of regional fishery resources. The regular collection of data permits to organize and harmonize the observation of the fishing activities, to manage the whole of the tasks necessary for an efficient system of observation, to harmonize fisheries observation on a national scale, to make quality data available to the Institute's teams through efficient extraction tools, to support research programs, resource assessments and fisheries expertise, notably in support of public policies, the development of integrated indicators and summaries on fisheries for research, fishermen, managers and the general public. The training of FIS agents permits to engage a field team through the mandatory data collection for the European Commission and to ensure enough data quality to produce Marine Natural Park performance indicators.

Keywords: FIS, DCF, indicators, fisheries, management

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Seabird-based tourism: a rising industry and new challenges for seabird islands

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The tourism industry generates more than 300 million jobs worldwide and contributes to the growth of the gross domestic product in many island territories. Natural heritage sites offer opportunities for nature-based tourism in these territories, so that it is currently considered the fastest growing segment of the tourism market. The growing societal demand for this type of tourism raises the question of its ecological impacts. As pointed out by the latest World Ocean Assessment, seabirds figure increasingly among the candidate species for nature-based tourism worldwide. Seabirds are often large, elegant, colorful and spectacular species which can be observed in large colonies in remote natural areas. However, this animal group is declining and it is threatened at a global level. The importance of seabirds as indicators of the quality of both marine and terrestrial habitats as well as their important role as ecosystem engineers highlights a topical conservation challenge in their use as a touristic product. The objectives of this study are: i) to review the literature on the impacts of tourism on seabirds and on their habitats; and ii) to highlight future research fronts that will contribute to a better understanding and mitigation of these impacts. Relevant information suggests that the magnitude of the effects induced by humans visiting seabird colonies may vary with the number of people, the frequency of visits, the type of activity, but also between species and with the phase of the breeding cycle. Impacts can be direct or indirect and they can be immediate or delayed and affect seabird physiology, ecology, dynamics or behavior. Behavioral ecology approaches such as flight initiation distances, and fear landscape may provide information directly relevant to managers. We also suggest that multidisciplinary approaches (behavior and physiology, socio-economics, economy...) are needed to better understand animal sensitivity, expectations from tourists, and help evaluate the conservation and economic benefits if any.

Keywords: seabird, nature based tourism, conservation, islands, man nature coexistence

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[*] Speaker

Species interactions / Networks / Trophic Ecology

Contents

Flowers visited by *Rousettus madagascariensis* (Chiroptera: Pteropodidae) in the Réserve Spéciale d'Ankarana (Madagascar)

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Old World fruit bats (Pteropodidae) are potential pollinators of different flowering plants, which they use as food resources. While information on the plants visited by the two largest endemic species of Malagasy pteropodids, *Pteropus rufus* and *Eidolon dupreanum*, are available, such details on those visited by *Rousettus madagascariensis*, the smallest endemic species, are few. The objective of this study was to identify the flowering plants visited by *R. madagascariensis* in the Réserve Spéciale d'Ankarana, northern Madagascar. Individual bats were captured during the dry (September and November 2016) and wet seasons (April 2017) as they entered the cave day-roost before dawn. Immediately after capture, the rostrum of each bats was swabbed for traces of pollen, which were in turn identified using a flowering plant pollen catalog for the site. Thirteen plant taxa were identified from the swabs, five of which are exotic. *Parkia madagascariensis* (26.5%) *and Capurodendron ankaranense* (10.9%) were the most important native species visited; *Eucalyptus* spp. (16.9%) and *Ceiba pentandra* (7.2%) were the most important non-native visited. Female and male of *Rousettus madagascariensi*s showed different preferences for plants during the two seasons. Regardless of the plant species, both males and females showed preferences for small, white or yellow flowers, with numerous stamens and axillary floriferous branches, which represent chiropterophilic traits. It is assumed that *R. madagascariensis* may be responsible for the pollination of some of the plants visited, which included native and non-native species.

Keywords: Ankarana, flowers visited, fruit bat, pollen, swabs

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Frugivory and seed dispersal of endemic Malagasy baobabs after megafauna extinction

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Frugivory is a key plant-animal interaction. Large seeds are dispersed by large frugivores called megafauna. The extinction of megafauna can therefore affect the survival of large seeded-plants. This is the case of the endemic Malagasy baobab, *Adansonia rubrostipa* Jum & Perr, whose fruit traits are suited to be dispersed by extinct megafauna like giant lemurs, giant tortoises and elephant birds. In fact, baobab trees produce unusual large fruits and appear to have no extant native seed disperser. We suggest that the quantity of baobabs seeds dispersed in the forest has been reduced as current frugivores are unable to break baobabs fruits and disperse their seeds. The current native frugivore visitors of *Adansonia rubrostipa* in the western dry forest of Morondava, Madagascar are analyzed using fields measurements. We chose a population of 200 focal fruiting trees to monitor fallen baobab fruits located beneath those trees. We made diurnal and nocturnal observations using binoculars and animal identification from tooth marks found on gnawed fruits to describe potential seed dispersers *versus* seed predators. The results showed that no significant native frugivores that consume *Adansonia rubrostipa* fruits were observed. A higher proportion of mature fruits remained intact and rotten on the ground, compared to opened and gnawed fruits (Chi square test: 170.557, $p < 0.0001$). The giant rat, *Hypogeomus antimena*, was observed to manipulate mature fruits but could not be considered as a legitimate seed disperser. Incisor marks on gnawed fruits revealed that the native rat, *Eliurus muxinus*, could potentially be a baobab seed predator. Our findings suggest that Malagasy baobab species are vulnerable to the loss of primary seed dispersers. This could affect the seedling establishment and thus impede the recruitment of Malagasy baobab trees.

Keywords: Adansonia, anachronism, seed, dispersal, megafauna, Madagascar

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The relative role of frugivore pigeons as seed dispersers on oceanic islands: a key ecosystem function

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The simplicity of insular communities implies less functional redundancy compared to analogous assemblages on the mainland. This has important implications for island conservation since the disappearance of one species could lead to the loss of its function in the ecosystem. Fruit-eating animals are key elements in many ecosystems, performing essential functions such as seed dispersal. Due to the frequent absence of large-bodied mammals on oceanic islands, these frugivore assemblages tend to be dominated by large birds such as pigeons and doves (Columbidae, hereinafter 'pigeons'). This family is widely distributed on (sub)tropical islands, where they also are highly threatened. In this contribution we aim to assess the role of frugivore pigeons as seed dispersers on islands, especially those oceanic ones. To that end, we carried out a comprehensive literature review focused in qualitative components of seed dispersal (seed treatment, seed size and dispersal distance). Moreover, we used a large previously constructed database of 74 tropical and subtropical islands within 20 archipelagos to evaluate the relative importance of these birds in oceanic island ecosystems according to significant features in frugivore assemblages (body mass, fruit proportion in diet, and size of frugivore community). We highlight that island frugivore pigeons provide important –but understudied– ecological services such as large-seeded plant dispersal or long-distance dispersal, essential to the persistence of the forests they inhabit. Pigeons occupy the first place in the relative importance ranking (above passerines, fruit bats, parrots, lizards, tortoises, etc.) of almost 1,200 global records of oceanic island seed dispersers. Since these services are often irreplaceable on oceanic islands, conservation and recovery of the frugivorous pigeon populations should be considered an important milestone to ensure restoration of insular ecosystems and their self-sustainability, particularly on remote islands in the Pacific Ocean.

Keywords: seed dispersal, pigeons, oceanic islands, frugivore assemblages, island conservation

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Evolution of large flowers adapted to small pollinators in oceanic islands

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Oceanic islands generally lack larger pollinators with longer proboscis compared to continents and continental islands. In oceanic islands, the disappearance of long-tongued pollinators often causes higher dominance of small pollinators with shorter proboscis. The dominance of short-tongued pollinators is expected to influence the evolution of flower size and morphology in plants with specialized floral organs, such as long corolla tube and spur. Such plant species generally have smaller flowers in oceanic islands than in continental islands. However, we found that *Calystegia soldanella* flowers were larger in oceanic islands than in continental islands. In this study, we examine an adaptive significance of the larger oceanic flowers of *C. soldanella* by comparing floral organ sizes, pollinator composition and the relationship between flower size and pollination success between oceanic and continental populations. We investigated lengths of petal, corolla tube, style and stamens, pollinator species and pollen receipt and removal success of *C. soldanella* at three coastal sites in the Honshu island, the largest continental island of Japan, and at a single site in each of five oceanic islands belong to the Izu (oceanic) islands in 2013, 2014, 2017 and 2018. We found that oceanic populations have significantly larger petals and longer pistils than continental populations. In continental islands, flowers were mainly visited by large bees such as bumble bees, whereas flowers were more frequently visited by small bees in oceanic islands. Pollination success increased with petal size in both island types. The trend was more remarkable in oceanic populations than in continental ones. Although the pistil length was positively correlated with pollination success in oceanic populations, the relationship was negative in continental populations. Large bees commonly landed on the petals and filaments, whereas small pollinators often landed directly on the stigmas. The findings suggest that the larger petal attracted more small bees and the longer pistils would better function as their landing sites to increase pollination success in oceanic islands.

Keywords: pollination, floral evolution, Calystegia soldanella, proboscis length, Izu islands

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Japanese wood pigeon as a potential inter-island seed disperser in Izu island chain in Japan, indicated by its diet and seasonal movement pattern

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Long-distance seed dispersal among islands is essential for vegetation development in oceanic island ecosystems. Pigeons possibly contribute to long-distance seed dispersal in tropical oceanic islands due to their large body size, strong flying capacity and relatively long gut-passage time. The Japanese wood pigeon *Columba janthina* is distributed across remote islands around the Japanese main islands and Korean Peninsula. This pigeon is thought to be a seed predator, but some small seeds (< 3 mm in diameter) have been found to remain in their feces. Recent studies based on direct observations and genetic analyses conducted in Ogasawara island chain in Japan indicated the pigeons were highly mobile and can fly among islands up to 150 km apart. To estimate the potential of the Japanese wood pigeon as a long-distance deed disperser, we observed their seasonal movement pattern between Hachijojima and Hachijo-Kojima in Izu island chain. We also estimated their diet and food resource availability in each island habitat. More than 3,000 pigeons at a maximum can move between islands approximately 4 km apart within a day. The number of individuals moving between islands dramatically fluctuated among seasons, increased in summer and decreased in winter. Seeds of several plants such as Morus spp. remained in their feces when many pigeons moved between the islands. The movement pattern of the pigeon might be related to their breeding cycle and food resource availability in each island and may only affect inter island dispersal of plants that produce fruits in summer. To understand the ecological function of highly mobile island pigeons, detection of direct evidence of inter-island seed dispersal and its effects on population structure of seed plants are future challenges.

Keywords: *Columba janthina*, inter island movement, Izu islands, seed dispersal

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[*] Speaker

Experimental removal of dominant plants alters the diversity of a network of flower-visiting insects

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Plants form the base of complex communities on terrestrial ecosystems, and are the basic resource for insect herbivores and their associated natural enemies. Most plants contain flowers, and important interactions occur in these organs. Many insects are flower visitors and are known to be affected by habitat loss, fragmentation, and changes in landscape structure, but few studies have experimentally tested how habitat loss alters the structure of flower-visiting insect communities.In this study we focused on thrips (Insecta: Thysanoptera) as a model system. Previous studies in Reunion have revealed that flowers of the following exotic plants species host highly diverse communities of flower-visiting thrips : *Solanum mauritianum*, *Lantana camara*, *Ipomea indica.* Here, we tested the hypothesis that elimination of *S. mauritianum* flowers (as an important habitat for adult thrips) will trigger changes in thrips communities in the other two plants.We established replicated communities involving the three plants, and in a paired design, *S. mauritanicum* flowers were eliminated or not. The effect of this treatment on thrips was assessed during one month, by estimating their abundance, richness (i.e. the number of species) and diversity (shanon and simpson indexes). A community of eleven native and exotic thrips species was found. The treatment did not have any effect on insect abundance or diversity, but it had an effect on richness: elimination of *S. mauritianum* flowers had a negative effect on the richness of the number of species found on *L. camara,* but not on *I. indica.* At the landscape level, we observed that both the proportion of sugarcane and habitat fragmentation correlated with thrips richness. These correlations, however, were only observed when *S. mauritianum* flowers were eliminated, and not in our controls. Although our study was performed on exotic plant species, we provide evidence that at a fine spatial scale, the loss of a plant species that hosts a large diversity of flower-visiting insects can have consequences that cascade to the community of insects inhabiting other plants. Future studies are needed to unveil whether similar effects occur in communities of non-exotic plants, and to explore the consequences of habitat loss at a larger scale.

Keywords: flower visitors, thrips, habitat loss, insect diversity, habitat fragmentation

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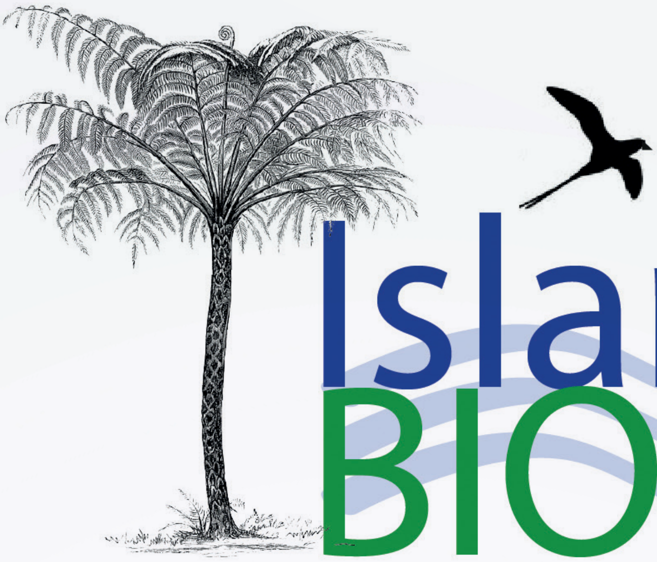
Author Index



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